



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: MIYAZONO, Kohei  
TEN DIJKE, Peter  
FRANZEN, Petra  
YAMASHITA, Hidetoshi  
HELDIN, Carl-Henrik
- (ii) TITLE OF INVENTION: ACTIVIN RECEPTOR LIKE KINASES, PROTEINS  
HAVING SERINE THREONINE KINASE DOMAINS,  
AND THEIR USE
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
  - (B) STREET: 666 Fifth Avenue
  - (C) CITY: New York City
  - (D) STATE: New York
  - (E) COUNTRY: USA
  - (F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette, 3.25 inch, 1.44mb
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: PC-DOS
  - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/906,068
  - (B) FILING DATE: July 11, 2001
- (vii) PRIOR APPLICATION DATE:
  - (A) APPLICATION NUMBER: 08/436,265
  - (B) FILING DATE: October 30, 1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/GB93/02367
  - (B) FILING DATE: November 17, 1993
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: GB 9224057.1
  - (B) FILING DATE: November 17, 1992
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: GB 9304677.9
  - (B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: GB 9304680.3
  - (B) FILING DATE: March 8, 1993
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 9311047.6
  - (B) FILING DATE: May 28, 1993

- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: 9313763.6  
 (B) FILING DATE: July 2, 1993
- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: 9316099.2  
 (B) FILING DATE: August 3, 1993
- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: 321344.5  
 (B) FILING DATE: October 15, 1993
- (viii) ATTORNEY/AGENT INFORMATION:  
 (A) NAME: Norman D. Hanson  
 (B) REGISTRATION NUMBER: 30,946  
 (C) REFERENCE/DOCKET NUMBER: LUD 5298.4 DIV (10105901)
- (ix) TELECOMMUNICATION INFORMATION:  
 (A) TELEPHONE: (212) 318-3000  
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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1984 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: unknown  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Homo sapiens

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 283..1791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA	60
AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC	120
GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT	180
CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA	240
AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC	294
Met Thr Leu Gly	
1	
TCC CCC AGG AAA GGC CTT CTG ATG CTG CTG ATG GCC TTG GTG ACC CAG	342
Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln	
5 10 15 20	
GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT	390
Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val Thr Cys Thr Cys	
25 30 35	
GAG AGC CCA CAT TGC AAG GGG CCT ACC TGC CGG GGG GCC TGG TGC ACA	438
Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly Ala Trp Cys Thr	
40 45 50	
GTA GTG CTG GTG CGG GAG GAG GGG AGG CAC CCC CAG GAA CAT CGG GGC	486
Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln Glu His Arg Gly	
55 60 65	

TGC GGG AAC TTG CAC AGG GAG CTC TGC AGG GGG CGC CCC ACC GAG TTC	534
Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg Pro Thr Glu Phe	
70 75 80	
GTC AAC CAC TAC TGC TGC GAC AGC CAC CTC TGC AAC CAC AAC GTG TCC	582
Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn His Asn Val Ser	
85 90 95 100	
CTG GTG CTG GAG GCC ACC CAA CCT CCT TCG GAG CAG CCG GGA ACA GAT	630
Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln Pro Gly Thr Asp	
105 110 115	
GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG	678
Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu	
120 125 130	
GTG GCC CTG GGT GTC CTG GGC CTG TGG CAT GTC CGA CGG AGG CAG GAG	726
Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg Arg Arg Gln Glu	
135 140 145	
AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG	774
Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu	
150 155 160	
AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT	822
Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser	
165 170 175 180	
GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG	870
Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg	
185 190 195	
ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC	918
Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	
200 205 210	
TAT GGC GAA GTG TGG CGG GGC TTG TGG CAC GGT GAG AGT GTG GCC GTC	966
Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu Ser Val Ala Val	
215 220 225	
AAG ATC TTC TCC TCG AGG GAT GAA CAG TCC TGG TTC CGG GAG ACT GAG	1014
Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg Glu Thr Glu	
230 235 240	
ATC TAT AAC ACA GTA TTG CTC AGA CAC GAC AAC ATC CTA GGC TTC ATC	1062
Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu Gly Phe Ile	
245 250 255 260	
GCC TCA GAC ATG ACC TCC CGC AAC TCG AGC ACG CAG CTG TGG CTC ATC	1110
Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu Trp Leu Ile	
265 270 275	
ACG CAC TAC CAC GAG CAC GGC TCC CTC TAC GAC TTT CTG CAG AGA CAG	1158
Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu Gln Arg Gln	
280 285 290	
ACG CTG GAG CCC CAT CTG GCT CTG AGG CTA GCT GTG TCC GCG GCA TGC	1206
Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val Ser Ala Ala Cys	
295 300 305	
GGC CTG GCG CAC CTG CAC GTG GAG ATC TTC GGT ACA CAG GGC AAA CCA	1254
Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln Gly Lys Pro	
310 315 320	
GCC ATT GCC CAC CGC GAC TTC AAG AGC CGC AAT GTG CTG GTC AAG AGC	1302
Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val Leu Val Lys Ser	
325 330 335 340	
AAC CTG CAG TGT TGC ATC GCC GAC CTG GGC CTG GCT GTG ATG CAC TCA	1350
Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Met His Ser	
345 350 355	
CAG GGC AGC GAT TAC CTG GAC ATC GGC AAC AAC CCG AGA GTG GGC ACC	1398
Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro Arg Val Gly Thr	
360 365 370	

AAG CGG TAC ATG GCA CCC GAG GTG CTG GAC GAG CAG ATC CGC ACG GAC	1446
Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln Ile Arg Thr Asp	
375 380 385	
TGC TTT GAG TCC TAC AAG TGG ACT GAC ATC TGG GCC TTT GGC CTG GTG	1494
Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe Gly Leu Val	
390 395 400	
CTG TGG GAG ATT GCC CGC CGG ACC ATC GTG AAT GGC ATC GTG GAG GAC	1542
Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly Ile Val Glu Asp	
405 410 415 420	
TAT AGA CCA CCC TTC TAT GAT GTG GTG CCC AAT GAC CCC AGC TTT GAG	1590
Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp Pro Ser Phe Glu	
425 430 435	
GAC ATG AAG AAG GTG GTG TGT GTG GAT CAG CAG ACC CCC ACC ATC CCT	1638
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Ile Pro	
440 445 450	
AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG	1686
Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	
455 460 465	
CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG	1734
Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg	
470 475 480	
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA	1782
Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys	
485 490 495 500	
GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC	1831
Val Ile Gln	
TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG	1891
TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCACCC AGCCAAAAAT	1951
ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA	1984

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala	
1 5 10 15	
Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val	
20 25 30	
Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly	
35 40 45	
Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln	
50 55 60	
Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg	
65 70 75 80	
Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn	
85 90 95	
His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln	
100 105 110	
Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
115 120 125	
Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
130 135 140	

Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser  
 145 150 155 160  
 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp  
 165 170 175  
 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe  
 180 185 190  
 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val  
 195 200 205  
 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu  
 210 215 220  
 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe  
 225 230 235 240  
 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile  
 245 250 255  
 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln  
 260 265 270  
 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe  
 275 280 285  
 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val  
 290 295 300  
 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr  
 305 310 315 320  
 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val  
 325 330 335  
 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala  
 340 345 350  
 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro  
 355 360 365  
 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln  
 370 375 380  
 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala  
 385 390 395 400  
 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly  
 405 410 415  
 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp  
 420 425 430  
 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr  
 435 440 445  
 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu  
 450 455 460  
 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu  
 465 470 475 480  
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro  
 485 490 495  
 Glu Lys Pro Lys Val Ile Gln  
 500

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2724 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 104..1630

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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CTCCGAGTAC CCCAGTGACC AGAGTGAGAG AAGCTCTGAA CGAGGGCACG CGGCTTGAAG      60
GACTGTGGGC AGATGTGACC AAGAGCCTGC ATTAAGTTGT ACA ATG GTA GAT GGA      115
                               Met Val Asp Gly
                               1
GTG ATG ATT CTT CCT GTG CTT ATC ATG ATT GCT CTC CCC TCC CCT AGT      163
Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
   5               10               15               20
ATG GAA GAT GAG AAG CCC AAG GTC AAC CCC AAA CTC TAC ATG TGT GTG      211
Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
               25               30               35
TGT GAA GGT CTC TCC TGC GGT AAT GAG GAC CAC TGT GAA GGC CAG CAG      259
Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
               40               45               50
TGC TTT TCC TCA CTG AGC ATC AAC GAT GGC TTC CAC GTC TAC CAG AAA      307
Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
               55               60               65
GGC TGC TTC CAG GTT TAT GAG CAG GGA AAG ATG ACC TGT AAG ACC CCG      355
Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
               70               75               80
CCG TCC CCT GGC CAA GCT GTG GAG TGC TGC CAA GGG GAC TGG TGT AAC      403
Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
   85               90               95               100
AGG AAC ATC ACG GCC CAG CTG CCC ACT AAA GGA AAA TCC TTC CCT GGA      451
Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
               105               110               115
ACA CAG AAT TTC CAC TTG GAG GTT GGC CTC ATT ATT CTC TCT GTA GTG      499
Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
               120               125               130
TTC GCA GTA TGT CTT TTA GCC TGC CTG CTG GGA GTT GCT CTC CGA AAA      547
Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
               135               140               145
TTT AAA AGG CGC AAC CAA GAA CGC CTC AAT CCC CGA GAC GTG GAG TAT      595
Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
               150               155               160
GGC ACT ATC GAA GGG CTC ATC ACC ACC AAT GTT GGA GAC AGC ACT TTA      643
Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
   165               170               175               180
GCA GAT TTA TTG GAT CAT TCG TGT ACA TCA GGA AGT GGC TCT GGT CTT      691
Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
               185               190               195
CCT TTT CTG GTA CAA AGA ACA GTG GCT CGC CAG ATT ACA CTG TTG GAG      739
Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
               200               205               210
TGT GTC GGG AAA GGC AGG TAT GGT GAG GTG TGG AGG GGC AGC TGG CAA      787
Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp Gln
               215               220               225
GGG GAA AAT GTT GCC GTG AAG ATC TTC TCC TCC CGT GAT GAG AAG TCA      835
Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Lys Ser
               230               235               240
TGG TTC AGG GAA ACG GAA TTG TAC AAC ACT GTG ATG CTG AGG CAT GAA      883
Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met Leu Arg His Glu
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245	AAT ATC TTA GGT TTC ATT GCT TCA GAC ATG ACA TCA AGA CAC TCC AGT	250	Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg His Ser Ser	255	260	931
	265	270	275			
ACC CAG CTG TGG TTA ATT ACA CAT TAT CAT GAA ATG GGA TCG TTG TAC						979
Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met Gly Ser Leu Tyr						
280	285	290				
GAC TAT CTT CAG CTT ACT ACT CTG GAT ACA GTT AGC TGC CTT CGA ATA						1027
Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser Cys Leu Arg Ile						
295	300	305				
GTG CTG TCC ATA GCT AGT GGT CTT GCA CAT TTG CAC ATA GAG ATA TTT						1075
Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His Ile Glu Ile Phe						
310	315	320				
GGG ACC CAA GGG AAA CCA GCC ATT GCC CAT CGA GAT TTA AAG AGC AAA						1123
Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys						
325	330	335	340			
AAT ATT CTG GTT AAG AAG AAT GGA CAG TGT TGC ATA GCA GAT TTG GGC						1171
Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile Ala Asp Leu Gly						
345	350	355				
CTG GCA GTC ATG CAT TCC CAG AGC ACC AAT CAG CTT GAT GTG GGG AAC						1219
Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu Asp Val Gly Asn						
360	365	370				
AAT CCC CGT GTG GGC ACC AAG CGC TAC ATG GCC CCC GAA GTT CTA GAT						1267
Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp						
375	380	385				
GAA ACC ATC CAG GTG GAT TGT TTC GAT TCT TAT AAA AGG GTC GAT ATT						1315
Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys Arg Val Asp Ile						
390	395	400				
TGG GCC TTT GGA CTT GTT TTG TGG GAA GTG GCC AGG CGG ATG GTG AGC						1363
Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg Arg Met Val Ser						
405	410	415	420			
AAT GGT ATA GTG GAG GAT TAC AAG CCA CCG TTC TAC GAT GTG GTT CCC						1411
Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr Asp Val Val Pro						
425	430	435				
AAT GAC CCA AGT TTT GAA GAT ATG AGG AAG GTA GTC TGT GTG CAA						1459
Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val Cys Val Asp Gln						
440	445	450				
CAA AGG CCA AAC ATA CCC AAC AGA TGG TTC TCA GAC CCG ACA TTA ACC						1507
Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp Pro Thr Leu Thr						
455	460	465				
TCT CTG GCC AAG CTA ATG AAA GAA TGC TGG TAT CAA AAT CCA TCC GCA						1555
Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln Asn Pro Ser Ala						
470	475	480				
AGA CTC ACA GCA CTG CGT ATC AAA AAG ACT TTG ACC AAA ATT GAT AAT						1603
Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr Lys Ile Asp Asn						
485	490	495	500			
TCC CTC GAC AAA TTG AAA ACT GAC TGT TGACATTTTC ATAGTGTCAA						1650
Ser Leu Asp Lys Leu Lys Thr Asp Cys						
505						
GAAGGAAGAT TTGACGTTGT TGTCATTGTC CAGCTGGGAC CTAATGCTGG CCTGACTGGT						1710
TGTCAGAATG GAATCCATCT GTCTCCCTCC CCAAATGGCT GCTTTGACAA GGCAGACGTC						1770
GTACCCAGCC ATGTGTTGGG GAGACATCAA AACCACCCTA ACCTCGCTCG ATGACTGTGA						1830
ACTGGGCATT TCACGAAGT TTACACTGC AGAGACTAAT GTTGGACAGA CACTGTTGCA						1890
AAGGTAGGGA CTGGAGGAAC ACAGAGAAAT CCTAAAAGAG ATCTGGGCAT TAAGTCAGTG						1950
GCTTTGCATA GCTTTCACAA GTCTCCTAGA CACTCCCCAC GGGAAACTCA AGGAGGTGGT						2010
GAATTTTAA TCAGCAATAT TGCCTGTGCT TCTCTTCTTT ATTGCACTAG GAATTCTTTG						2070
CATTCCTTAC TTGCACTGTT ACTCTTAATT TTAAAGACCC AACTTGCCAA AATGTTGGCT						2130

GCGTACTCCA	CTGGTCTGTC	TTTGGATAAT	AGGAATTCAA	TTTGGCAAAA	CAAAATGTAA	2190
TGTCAGACTT	TGCTGCATTT	TACACATGTG	CTGATGTTTA	CAATGATGCC	GAACATTAGG	2250
AATTGTTTAT	ACACAACTTT	GCAAATTATT	TATTACTTGT	GCACTTAGTA	GTTTTTACAA	2310
AACTGCTTTG	TGCATATGTT	AAAGCTTATT	TTTATGTGGT	CTTATGATTT	TATTACAGAA	2370
ATGTTTTTAA	CACTATACTC	TAAAATGGAC	ATTTTCTTTT	ATTATCAGTT	AAAATCACAT	2430
TTTAAGTGCT	TCACATTTGT	ATGTGTGTAG	ACTGTAACTT	TTTTTCAGTT	CATATGCAGA	2490
ACGTATTTAG	CCATTACCCA	CGTGACACCA	CCGAATATAT	TATCGATTTA	GAAGCAAAGA	2550
TTTCAGTAGA	ATTTTAGTCC	TGAACGCTAC	GGGGAAAATG	CATTTTCTTC	AGAATTATCC	2610
ATTACGTGCA	TTTAAACTCT	GCCAGAAAAA	AATAACTATT	TTGTTTAAAT	CTACTTTTTG	2670
TATTTAGTAG	TTATTTGTAT	AAATTAAATA	AACTGTTTTT	AAGTCAAAAA	AAAA	2724

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 509 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Val	Asp	Gly	Val	Met	Ile	Leu	Pro	Val	Leu	Ile	Met	Ile	Ala	Leu
1				5					10					15	
Pro	Ser	Pro	Ser	Met	Glu	Asp	Glu	Lys	Pro	Lys	Val	Asn	Pro	Lys	Leu
				20				25					30		
Tyr	Met	Cys	Val	Cys	Glu	Gly	Leu	Ser	Cys	Gly	Asn	Glu	Asp	His	Cys
				35				40					45		
Glu	Gly	Gln	Gln	Cys	Phe	Ser	Ser	Leu	Ser	Ile	Asn	Asp	Gly	Phe	His
				50				55				60			
Val	Tyr	Gln	Lys	Gly	Cys	Phe	Gln	Val	Tyr	Glu	Gln	Gly	Lys	Met	Thr
				65				70				75			80
Cys	Lys	Thr	Pro	Pro	Ser	Pro	Gly	Gln	Ala	Val	Glu	Cys	Cys	Gln	Gly
				85				90						95	
Asp	Trp	Cys	Asn	Arg	Asn	Ile	Thr	Ala	Gln	Leu	Pro	Thr	Lys	Gly	Lys
				100				105						110	
Ser	Phe	Pro	Gly	Thr	Gln	Asn	Phe	His	Leu	Glu	Val	Gly	Leu	Ile	Ile
				115				120					125		
Leu	Ser	Val	Val	Phe	Ala	Val	Cys	Leu	Leu	Ala	Cys	Leu	Leu	Gly	Val
				130				135				140			
Ala	Leu	Arg	Lys	Phe	Lys	Arg	Arg	Asn	Gln	Glu	Arg	Leu	Asn	Pro	Arg
				145				150				155			160
Asp	Val	Glu	Tyr	Gly	Thr	Ile	Glu	Gly	Leu	Ile	Thr	Thr	Asn	Val	Gly
				165				170						175	
Asp	Ser	Thr	Leu	Ala	Asp	Leu	Leu	Asp	His	Ser	Cys	Thr	Ser	Gly	Ser
				180				185					190		
Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Ile
				195				200					205		
Thr	Leu	Leu	Glu	Cys	Val	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg
				210				215				220			
Gly	Ser	Trp	Gln	Gly	Glu	Asn	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg
				225				230				235			240
Asp	Glu	Lys	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Leu	Tyr	Asn	Thr	Val	Met
				245				250						255	
Leu	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser
				260				265					270		
Arg	His	Ser	Ser	Thr	Gln	Leu	Trp	Leu	Ile	Thr	His	Tyr	His	Glu	Met
				275				280					285		
Gly	Ser	Leu	Tyr	Asp	Tyr	Leu	Gln	Leu	Thr	Thr	Leu	Asp	Thr	Val	Ser
				290				295					300		

Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His  
 305 310 315 320  
 Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp  
 325 330 335  
 Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile  
 340 345 350  
 Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu  
 355 360 365  
 Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro  
 370 375 380  
 Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys  
 385 390 395 400  
 Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg  
 405 410 415  
 Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr  
 420 425 430  
 Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val  
 435 440 445  
 Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp  
 450 455 460  
 Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln  
 465 470 475 480  
 Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr  
 485 490 495  
 Lys Ile Asp Asn Ser Leu Asp Lys Leu Lys Thr Asp Cys  
 500 505

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2932 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 310..1905

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GCTCCGCGCC GAGGGCTGGA GGATGCGTTC CCTGGGGTCC GGACTTATGA AAATATGCAT	60
CAGTTTAATA CTGTCTTGGA ATTCATGAGA TGGAAGCATA GGTCAAAGCT GTTTGGAGAA	120
AATCAGAAGT ACAGTTTTAT CTAGCCACAT CTTGGAGGAG TCGTAAGAAA GCAGTGGGAG	180
TTGAAGTCAT TGTCAAGTGC TTGCGATCTT TTACAAGAAA ATCTCACTGA ATGATAGTCA	240
TTTAAATTGG TGAAGTAGCA AGACCAATTA TTAAAGGTGA CAGTACACAG GAAACATTAC	300
AATTGAACA ATG ACT CAG CTA TAC ATT TAC ATC AGA TTA TTG GGA GCC	348
Met Thr Gln Leu Tyr Ile Tyr Ile Arg Leu Leu Gly Ala	
1 5 10	
TAT TTG TTC ATC ATT TCT CGT GTT CAA GGA CAG AAT CTG GAT AGT ATG	396
Tyr Leu Phe Ile Ile Ser Arg Val Gln Gly Gln Asn Leu Asp Ser Met	
15 20 25	
CTT CAT GGC ACT GGG ATG AAA TCA GAC TCC GAC CAG AAA AAG TCA GAA	444
Leu His Gly Thr Gly Met Lys Ser Asp Ser Asp Gln Lys Lys Ser Glu	

30	AAT GGA GTA ACC TTA GCA CCA GAG GAT ACC TTG CCT TTT TTA AAG TGC	45	492
	Asn Gly Val Thr Leu Ala Pro Glu Asp Thr Leu Pro Phe Leu Lys Cys		
	50	55	60
	TAT TGC TCA GGG CAC TGT CCA GAT GAT GCT ATT AAT AAC ACA TGC ATA		540
	Tyr Cys Ser Gly His Cys Pro Asp Asp Ala Ile Asn Asn Thr Cys Ile		
	65	70	75
	ACT AAT GGA CAT TGC TTT GCC ATC ATA GAA GAA GAT GAC CAG GGA GAA		588
	Thr Asn Gly His Cys Phe Ala Ile Ile Glu Glu Asp Asp Gln Gly Glu		
	80	85	90
	ACC ACA TTA GCT TCA GGG TGT ATG AAA TAT GAA GGA TCT GAT TTT CAG		636
	Thr Thr Leu Ala Ser Gly Cys Met Lys Tyr Glu Gly Ser Asp Phe Gln		
	95	100	105
	TGC AAA GAT TCT CCA AAA GCC CAG CTA CGC CGG ACA ATA GAA TGT TGT		684
	Cys Lys Asp Ser Pro Lys Ala Gln Leu Arg Arg Thr Ile Glu Cys Cys		
	110	115	120
	CGG ACC AAT TTA TGT AAC CAG TAT TTG CAA CCC ACA CTG CCC CCT GTT		732
	Arg Thr Asn Leu Cys Asn Gln Tyr Leu Gln Pro Thr Leu Pro Pro Val		
	130	135	140
	GTC ATA GGT CCG TTT TTT GAT GGC AGC ATT CGA TGG CTG GTT TTG CTC		780
	Val Ile Gly Pro Phe Phe Asp Gly Ser Ile Arg Trp Leu Val Leu Leu		
	145	150	155
	ATT TCT ATG GCT GTC TGC ATA ATT GCT ATG ATC ATC TTC TCC AGC TGC		828
	Ile Ser Met Ala Val Cys Ile Ile Ala Met Ile Ile Phe Ser Ser Cys		
	160	165	170
	TTT TGT TAC AAA CAT TAT TGC AAG AGC ATC TCA AGC AGA CGT CGT TAC		876
	Phe Cys Tyr Lys His Tyr Cys Lys Ser Ile Ser Ser Arg Arg Arg Tyr		
	175	180	185
	AAT CGT GAT TTG GAA CAG GAT GAA GCA TTT ATT CCA GTT GGA GAA TCA		924
	Asn Arg Asp Leu Glu Gln Asp Glu Ala Phe Ile Pro Val Gly Glu Ser		
	190	195	200
	CTA AAA GAC CTT ATT GAC CAG TCA CAA AGT TCT GGT AGT GGG TCT GGA		972
	Leu Lys Asp Leu Ile Asp Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly		
	210	215	220
	CTA CCT TTA TTG GTT CAG CGA ACT ATT GCC AAA CAG ATT CAG ATG GTC		1020
	Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val		
	225	230	235
	CGG CAA GTT GGT AAA GGC CGA TAT GGA GAA GTA TGG ATG GGC AAA TGG		1068
	Arg Gln Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp		
	240	245	250
	CGT GGC GAA AAA GTG GCG GTG AAA GTA TTC TTT ACC ACT GAA GAA GCC		1116
	Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala		
	255	260	265
	AGC TGG TTT CGA GAA ACA GAA ATC TAC CAA ACT GTG CTA ATG CGC CAT		1164
	Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His		
	270	275	280
	GAA AAC ATA CTT GGT TTC ATA GCG GCA GAC ATT AAA GGT ACA GGT TCC		1212
	Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser		
	290	295	300
	TGG ACT CAG CTC TAT TTG ATT ACT GAT TAC CAT GAA AAT GGA TCT CTC		1260
	Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu		
	305	310	315
	TAT GAC TTC CTG AAA TGT GCT ACA CTG GAC ACC AGA GCC CTG CTT AAA		1308
	Tyr Asp Phe Leu Lys Cys Ala Thr Leu Asp Thr Arg Ala Leu Leu Lys		
	320	325	330
	TTG GCT TAT TCA GCT GCC TGT GGT CTG TGC CAC CTG CAC ACA GAA ATT		1356
	Leu Ala Tyr Ser Ala Ala Cys Gly Leu Cys His Leu His Thr Glu Ile		

335		340		345		
TAT GGC ACC CAA GGA AAG CCC GCA ATT GCT CAT CGA GAC CTA AAG AGC						1404
Tyr Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser						
350		355		360		365
AAA AAC ATC CTC ATC AAG AAA AAT GGG AGT TGC TGC ATT GCT GAC CTG						1452
Lys Asn Ile Leu Ile Lys Lys Asn Gly Ser Cys Cys Ile Ala Asp Leu						
	370		375		380	
GGC CTT GCT GTT AAA TTC AAC AGT GAC ACA AAT GAA GTT GAT GTG CCC						1500
Gly Leu Ala Val Lys Phe Asn Ser Asp Thr Asn Glu Val Asp Val Pro						
	385		390		395	
TTG AAT ACC AGG GTG GGC ACC AAA CGC TAC ATG GCT CCC GAA GTG CTG						1548
Leu Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu						
	400		405		410	
GAC GAA AGC CTG AAC AAA AAC CAC TTC CAG CCC TAC ATC ATG GCT GAC						1596
Asp Glu Ser Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp						
	415		420		425	
ATC TAC AGC TTC GGC CTA ATC ATT TGG GAG ATG GCT CGT CGT TGT ATC						1644
Ile Tyr Ser Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile						
	430		435		440	445
ACA GGA GGG ATC GTG GAA GAA TAC CAA TTG CCA TAT TAC AAC ATG GTA						1692
Thr Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val						
	450		455		460	
CCG AGT GAT CCG TCA TAC GAA GAT ATG CGT GAG GTT GTG TGT GTC AAA						1740
Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys						
	465		470		475	
CGT TTG CGG CCA ATT GTG TCT AAT CGG TGG AAC AGT GAT GAA TGT CTA						1788
Arg Leu Arg Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu						
	480		485		490	
CGA GCA GTT TTG AAG CTA ATG TCA GAA TGC TGG GCC CAC AAT CCA GCC						1836
Arg Ala Val Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala						
	495		500		505	
TCC AGA CTC ACA GCA TTG AGA ATT AAG AAG ACG CTT GCC AAG ATG GTT						1884
Ser Arg Leu Thr Ala Lys Arg Ile Lys Lys Thr Leu Ala Lys Met Val						
	510		515		520	525
GAA TCC CAA GAT GTA AAA ATC TGATGGTTAA ACCATCGGAG GAGAACTCT						1935
Glu Ser Gln Asp Val Lys Ile						
	530					
AGACTGCAAG AACTGTTTTT ACCCATGGCA TGGGTGGAAT TAGAGTGGAA TAAGGATGTT						1995
AACTTGTTTC TCAGACTCTT TCTTCACTAC GTGTTACACAG GCTGCTAATA TTAAACCTTT						2055
CAGTACTCTT ATTAGGATAC AAGCTGGGAA CTTCTAAACA CTTTATTCTT TATATATGGA						2115
CAGCTTTATT TTAAATGTGG TTTTGTATGC CTTTTTTTAA GTGGGTTTTT ATGAACTGCA						2175
TCAAGACTTC AATCCTGATT AGTGTCTCCA GTCAAGCTCT GGGTACTGAA TTGCCTGTTC						2235
ATAAAACGGT GCTTTCTGTG AAAGCCTTAA GAAGATAAAT GAGCGCAGCA GAGATGGAGA						2295
AATAGACTTT GCCTTTTACC TGAGACATTC AGTTCGTTTG TATTCTACCT TTGTAAAACA						2355
GCCTATAGAT GATGATGTGT TTGGGATACT GCTTATTTTA TGATAGTTTG TCCTGTGTCC						2415
TTAGTGATGT GTGTGTGTCT CCATGCACAT GCACGCCGGG ATTCCTCTGC TGCCATTTGA						2475
ATTAGAAGAA AATAATTTAT ATGCATGCAC AGGAAGATAT TGGTGGCCGG TGGTTTTGTG						2535
CTTTAAAAAT GCAATATCTG ACCAAGATTC GCCAATCTCA TACAAGCCAT TTTCTTTGCA						2595
AGTGAGATAG CTTCCCCACC AGCTTTATTT TTAAACATGA AAGCTGATGC CAAGGCCAAA						2655
AGAAGTTTAA AGCATCTGTA AATTTGGACT GTTTTCCTTC AACCACCATT TTTTTTGTGG						2715
TTATTATTTT TGTCACGGAA AGCATCCTCT CCAAAGTTGG AGCTTCTATT GCCATGAACC						2775
ATGCTTACAA AGAAAGCACT TCTTATTGAA GTGAATTCCT GCATTTGATA GCAATGTAAG						2835
TGCCTATAAC CATGTTCTAT ATTCTTTATT CTCAGTAACT TTTAAAAGGG AAGTTATTTA						2895
TATTTTGTGT ATAATGTGCT TTATTTGCAA ATCACCC						2932

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: prôtein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Thr	Gln	Leu	Tyr	Ile	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Tyr	Leu	Phe
1				5				10						15	
Ile	Ile	Ser	Arg	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly
			20					25					30		
Thr	Gly	Met	Lys	Ser	Asp	Ser	Asp	Gln	Lys	Lys	Ser	Glu	Asn	Gly	Val
		35					40					45			
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser
	50					55					60				
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly
65					70					75				80	
His	Cys	Phe	Ala	Ile	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu
				85					90					95	
Ala	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp
			100					105					110		
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn
		115					120					125			
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly
	130					135					140				
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Leu	Leu	Ile	Ser	Met
145					150					155					160
Ala	Val	Cys	Ile	Ile	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
				165					170					175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Arg	Arg	Tyr	Asn	Arg	Asp
			180					185					190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
	195						200					205			
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
	210					215					220				
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225					230					235				240	
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
			245						250					255	
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
			260					265					270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
	275						280					285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
	290					295					300				
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305					310					315				320	
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
			325						330					335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
			340					345					350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
		355					360					365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
	370					375					380				
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Val	Pro	Leu	Asn	Thr
385					390					395				400	
Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser



Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val		
		115					120					125					
GGC	ATC	ATC	GCC	GGC	CCG	GTG	TTC	CTC	CTG	TTC	CTC	ATC	ATC	ATC	ATT	432	
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile		
		130					135					140					
GTT	TTC	CTT	GTC	ATT	AAC	TAT	CAT	CAG	CGT	GTC	TAT	CAC	AAC	CGC	CAG	480	
Val	Phe	Leu	Val	Ile	Asn	Tyr	His	Gln	Arg	Val	Tyr	His	Asn	Arg	Gln		
		145				150					155				160		
AGA	CTG	GAC	ATG	GAA	GAT	CCC	TCA	TGT	GAG	ATG	TGT	CTC	TCC	AAA	GAC	528	
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp		
			165						170					175			
AAG	ACG	CTC	CAG	GAT	CTT	GTC	TAC	GAT	CTC	TCC	ACC	TCA	GGG	TCT	GGC	576	
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly		
			180					185					190				
TCA	GGG	TTA	CCC	CTC	TTT	GTC	CAG	CGC	ACA	GTG	GCC	CGA	ACC	ATC	GTT	624	
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val		
		195					200					205					
TTA	CAA	GAG	ATT	ATT	GGC	AAG	GGT	CGG	TTT	GGG	GAA	GTA	TGG	CGG	GGC	672	
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly		
		210				215					220						
CGC	TGG	AGG	GGT	GGT	GAT	GTG	GCT	GTG	AAA	ATA	TTC	TCT	TCT	CGT	GAA	720	
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu		
		225			230				235					240			
GAA	CGG	TCT	TGG	TTC	AGG	GAA	GCA	GAG	ATA	TAC	CAG	ACG	GTC	ATG	CTG	768	
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu		
			245					250					255				
CGC	CAT	GAA	AAC	ATC	CTT	GGA	TTT	ATT	GCT	GCT	GAC	AAT	AAA	GAT	AAT	816	
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn		
		260				265						270					
GGC	ACC	TGG	ACA	CAG	CTG	TGG	CTT	GTT	TCT	GAC	TAT	CAT	GAG	CAC	GGG	864	
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly		
		275				280						285					
TCC	CTG	TTT	GAT	TAT	CTG	AAC	CGG	TAC	ACA	GTG	ACA	ATT	GAG	GGG	ATG	912	
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met		
		290				295					300						
ATT	AAG	CTG	GCC	TTG	TCT	GCT	GCT	AGT	GGG	CTG	GCA	CAC	CTG	CAC	ATG	960	
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met		
		305			310				315					320			
GAG	ATC	GTG	GGC	ACC	CAA	GGG	AAG	CCT	GGA	ATT	GCT	CAT	CGA	GAC	TTA	1008	
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu		
			325					330				335					
AAG	TCA	AAG	AAC	ATT	CTG	GTG	AAG	AAA	AAT	GGC	ATG	TGT	GCC	ATA	GCA	1056	
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala		
			340				345					350					
GAC	CTG	GGC	CTG	GCT	GTC	CGT	CAT	GAT	GCA	GTC	ACT	GAC	ACC	ATT	GAC	1104	
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp		
		355				360					365						
ATT	GCC	CCG	AAT	CAG	AGG	GTG	GGG	ACC	AAA	CGA	TAC	ATG	GCC	CCT	GAA	1152	
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu		
		370				375					380						
GTA	CTT	GAT	GAA	ACC	ATT	AAT	ATG	AAA	CAC	TTT	GAC	TCC	TTT	AAA	TGT	1200	
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys		
		385			390					395				400			
GCT	GAT	ATT	TAT	GCC	CTC	GGG	CTT	GTA	TAT	TGG	GAG	ATT	GCT	CGA	AGA	1248	
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg		
			405					410					415				
TGC	AAT	TCT	GGA	GGA	GTC	CAT	GAA	GAA	TAT	CAG	CTG	CCA	TAT	TAC	GAC	1296	

Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp	
			420					425					430			
TTA	GTG	CCC	TCT	GAC	CCT	TCC	ATT	GAG	GAA	ATG	CGA	AAG	GTT	GTA	TGT	1344
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys	
		435					440					445				
GAT	CAG	AAG	CTG	CGT	CCC	AAC	ATC	CCC	AAC	TGG	TGG	CAG	AGT	TAT	GAG	1392
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Ile	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu	
	450					455				460						
GCA	CTG	CGG	GTG	ATG	GGG	AAG	ATG	ATG	CGA	GAG	TGT	TGG	TAT	GCC	AAC	1440
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn	
	465				470				475					480		
GGC	GCA	GCC	CGC	CTG	ACG	GCC	CTG	CGC	ATC	AAG	AAG	ACC	CTC	TCC	CAG	1488
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln	
			485						490					495		
CTC	AGC	GTG	CAG	GAA	GAC	GTG	AAG	ATC	TA	ACT	GCTCC	CTCTCTCCAC				1535
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile								
			500				505									
ACGGAGCTCC	TGGCAGCGAG	AACTACGCAC	AGCTGCCGCG	TTGAGCGTAC	GATGGAGGCC											1595
TACCTCTCGT	TTCTGCCCAG	CCCTCTGTGG	CCAGGAGCCC	TGGCCCGCAA	GAGGGACAGA											1655
GCCCGGGAGA	GACTCGCTCA	CTCCCATGTT	GGGTTTGAGA	CAGACACCTT	TTCTATTTAC											1715
CTCCTAATGG	CATGGAGACT	CTGAGAGCGA	ATTGTGTGGA	GA	ACTCAGTG	CCACACCTCG										1775
AACTGGTTGT	AGTGGGAAGT	CCCGCGAAAC	CCGGTGCATC	TGGCACGTGG	CCAGGAGCCA											1835
TGACAGGGGC	GCTTGGGAGG	GGCCGGAGGA	ACCGAGGTGT	TGCCAGTGCT	AAGCTGCCCT											1895
GAGGGTTTCC	TTCGGGGACC	AGCCACAGC	ACACCAAGGT	GGCCCGGAAG	AACCAGAAGT											1955
GCAGCCCCTC	TCACAGGCAG	CTCTGAGCCG	CGCTTTCCCC	TCCTCCCTGG	GATGGACGCT											2015
GCCGGGAGAC	TGCCAGTGGA	GACGGAATCT	GCCGCTTTGT	CTGTCCAGCC	GTGTGTGCAT											2075
GTGCCGAGGT	GCGTCCCCCG	TTGTGCCTGG	TTCGTGCCAT	GCCCTTACAC	GTGCGTGTGA											2135
GTGTGTGTGT	GTGTCTGTAG	GTGCGCACTT	ACCTGCTTGA	GCTTTCTGTG	CATGTGCAGG											2195
TCGGGGGTGT	GGTCGTCATG	CTGTCCGTGC	TTGCTGGTGC	CTCTTTTCAG	TAGTGAGCAG											2255
CATCTAGTTT	CCCTGGTGCC	CTTCCCTGGA	GGTCTCTCCC	TCCCCCAGAG	CCCCTCATGC											2315
CACAGTGGA	CTCTGTGT															2333

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Met	Ala	Glu	Ser	Ala	Gly	Ala	Ser	Ser	Phe	Phe	Pro	Leu	Val	Val	Leu
1				5					10					15	
Leu	Leu	Ala	Gly	Ser	Gly	Gly	Ser	Gly	Pro	Arg	Gly	Val	Gln	Ala	Leu
		20						25				30			
Leu	Cys	Ala	Cys	Thr	Ser	Cys	Leu	Gln	Ala	Asn	Tyr	Thr	Cys	Glu	Thr
	35					40					45				
Asp	Gly	Ala	Cys	Met	Val	Ser	Phe	Phe	Asn	Leu	Asp	Gly	Met	Glu	His
	50					55				60					
His	Val	Arg	Thr	Cys	Ile	Pro	Lys	Val	Glu	Leu	Val	Pro	Ala	Gly	Lys
	65				70				75					80	
Pro	Phe	Tyr	Cys	Leu	Ser	Ser	Glu	Asp	Leu	Arg	Asn	Thr	His	Cys	Cys
			85					90					95		
Tyr	Thr	Asp	Tyr	Cys	Asn	Arg	Ile	Asp	Leu	Arg	Val	Pro	Ser	Gly	His
	100						105					110			
Leu	Lys	Glu	Pro	Glu	His	Pro	Ser	Met	Trp	Gly	Pro	Val	Glu	Leu	Val
	115					120					125				
Gly	Ile	Ile	Ala	Gly	Pro	Val	Phe	Leu	Leu	Phe	Leu	Ile	Ile	Ile	Ile

130	135	140
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln		
145	150	155
Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu Ser Lys Asp		160
	165	170
Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser Gly Ser Gly		175
	180	185
Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg Thr Ile Val		190
	195	200
Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val Trp Arg Gly		205
	210	215
Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser Ser Arg Glu		220
225	230	235
Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr Val Met Leu		240
	245	250
Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn Lys Asp Asn		255
	260	265
Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His Glu His Gly		270
	275	280
Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile Glu Gly Met		285
	290	295
Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His Leu His Met		300
305	310	315
Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His Arg Asp Leu		320
	325	330
Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys Ala Ile Ala		335
	340	345
Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp Thr Ile Asp		350
	355	360
Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu		365
370	375	380
Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser Phe Lys Cys		385
385	390	395
Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile Ala Arg Arg		400
	405	410
Cys Asn Ser Gly Gly Val His Glu Glu Tyr Gln Leu Pro Tyr Tyr Asp		415
	420	425
Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys Val Val Cys		430
	435	440
Asp Gln Lys Leu Arg Pro Asn Ile Pro Asn Trp Trp Gln Ser Tyr Glu		445
	450	455
Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp Tyr Ala Asn		460
465	470	475
Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln		480
	485	490
Leu Ser Val Gln Glu Asp Val Lys Ile		495
	500	505

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 77..1585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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GGCGAGGCGA GGTTCGCTGG GGTGAGGCAG CGGCGCGGCC GGGCCGGGCC GGGCCACAGG      60
CGGTGGCGGC GGGACC ATG GAG GCG GCG GTC GCT GCT CCG CGT CCC CGG      109
      Met Glu Ala Ala Val Ala Ala Pro Arg Pro Arg
              1              5              10
CTG CTC CTC CTC GTG CTG GCG GCG GCG GCG GCG GCG GCG GCG GCG CTG      157
Leu Leu Leu Leu Val Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Leu
              15              20              25
CTC CCG GGG GCG ACG GCG TTA CAG TGT TTC TGC CAC CTC TGT ACA AAA      205
Leu Pro Gly Ala Thr Ala Leu Gln Cys Phe Cys His Leu Cys Thr Lys
              30              35              40
GAC AAT TTT ACT TGT GTG ACA GAT GGG CTC TGC TTT GTC TCT GTC ACA      253
Asp Asn Phe Thr Cys Val Thr Asp Gly Leu Cys Phe Val Ser Val Thr
              45              50              55
GAG ACC ACA GAC AAA GTT ATA CAC AAC AGC ATG TGT ATA GCT GAA ATT      301
Glu Thr Thr Asp Lys Val Ile His Asn Ser Met Cys Ile Ala Glu Ile
              60              65              70              75
GAC TTA ATT CCT CGA GAT AGG CCG TTT GTA TGT GCA CCC TCT TCA AAA      349
Asp Leu Ile Pro Arg Asp Arg Pro Phe Val Cys Ala Pro Ser Ser Lys
              80              85              90
ACT GGG TCT GTG ACT ACA ACA TAT TGC TGC AAT CAG GAC CAT TGC AAT      397
Thr Gly Ser Val Thr Thr Thr Tyr Cys Cys Asn Gln Asp His Cys Asn
              95              100              105
AAA ATA GAA CTT CCA ACT ACT GTA AAG TCA TCA CCT GGC CTT GGT CCT      445
Lys Ile Glu Leu Pro Thr Thr Val Lys Ser Ser Pro Gly Leu Gly Pro
              110              115              120
GTG GAA CTG GCA GCT GTC ATT GCT GGA CCA GTG TGC TTC GTC TGC ATC      493
Val Glu Leu Ala Ala Val Ile Ala Gly Pro Val Cys Phe Val Cys Ile
              125              130              135
TCA CTC ATG TTG ATG GTC TAT ATC TGC CAC AAC CGC ACT GTC ATT CAC      541
Ser Leu Met Leu Met Val Tyr Ile Cys His Asn Arg Thr Val Ile His
              140              145              150              155
CAT CGA GTG CCA AAT GAA GAG GAC CCT TCA TTA GAT CGC CCT TTT ATT      589
His Arg Val Pro Asn Glu Glu Asp Pro Ser Leu Asp Arg Pro Phe Ile
              160              165              170
TCA GAG GGT ACT ACG TTG AAA GAC TTA ATT TAT GAT ATG ACA ACG TCA      637
Ser Glu Gly Thr Thr Leu Lys Asp Leu Ile Tyr Asp Met Thr Thr Ser
              175              180              185
GGT TCT GGC TCA GGT TTA CCA TTG CTT GTT CAG AGA ACA ATT GCG AGA      685
Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Arg
              190              195              200
ACT ATT GTG TTA CAA GAA AGC ATT GGC AAA GGT CGA TTT GGA GAA GTT      733
Thr Ile Val Leu Gln Glu Ser Ile Gly Lys Gly Arg Phe Gly Glu Val
              205              210              215
TGG AGA GGA AAG TGG CGG GGA GAA GAA GTT GCT GTT AAG ATA TTC TCC      781
Trp Arg Gly Lys Trp Arg Gly Glu Glu Val Ala Val Lys Ile Phe Ser
              220              225              230              235
TCT AGA GAA GAA CGT TCG TGG TTC CGT GAG GCA GAG ATT TAT CAA ACT      829
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr
              240              245              250
GTA ATG TTA CGT CAT GAA AAC ATC CTG GGA TTT ATA GCA GCA GAC AAT      877
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Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAC AAT GGT ACT TGG ACT CAG CTC TGG TTG GTG TCA GAT TAT CAT	925
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280	
GAG CAT GGA TCC CTT TTT GAT TAC TTA AAC AGA TAC ACA GTT ACT GTG	973
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Val	
285 290 295	
GAA GGA ATG ATA AAA CTT GCT CTG TCC ACG GCG AGC GGT CTT GCC CAT	1021
Glu Gly Met Ile Lys Leu Ala Leu Ser Thr Ala Ser Gly Leu Ala His	
300 305 310 315	
CTT CAC ATG GAG ATT GTT GGT ACC CAA GGA AAG CCA GCC ATT GCT CAT	1069
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Ala Ile Ala His	
320 325 330	
AGA GAT TTG AAA TCA AAG AAT ATC TTG GTA AAG AAG AAT GGA ACT TGC	1117
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys	
335 340 345	
TGT ATT GCA GAC TTA GGA CTG GCA GTA AGA CAT GAT TCA GCC ACA GAT	1165
Cys Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ser Ala Thr Asp	
350 355 360	
ACC ATT GAT ATT GCT CCA AAC CAC AGA GTG GGA ACA AAA AGG TAC ATG	1213
Thr Ile Asp Ile Ala Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met	
365 370 375	
GCC CCT GAA GTT CTC GAT GAT TCC ATA AAT ATG AAA CAT TTT GAA TCC	1261
Ala Pro Glu Val Leu Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser	
380 385 390 395	
TTC AAA CGT GCT GAC ATC TAT GCA ATG GGC TTA GTA TTC TGG GAA ATT	1309
Phe Lys Arg Ala Asp Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile	
400 405 410	
GCT CGA CGA TGT TCC ATT GGT GGA ATT CAT GAA GAT TAC CAA CTG CCT	1357
Ala Arg Arg Cys Ser Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAT GAT CTT GTA CCT TCT GAC CCA TCA GTT GAA GAA ATG AGA AAA	1405
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys	
430 435 440	
GTT GTT TGT GAA CAG AAG TTA AGG CCA AAT ATC CCA AAC AGA TGG CAG	1453
Val Val Cys Glu Gln Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln	
445 450 455	
AGC TGT GAA GCC TTG AGA GTA ATG GCT AAA ATT ATG AGA GAA TGT TGG	1501
Ser Cys Glu Ala Leu Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp	
460 465 470 475	
TAT GCC AAT GGA GCA GCT AGG CTT ACA GCA TTG CGG ATT AAG AAA ACA	1549
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
TTA TCG CAA CTC AGT CAA CAG GAA GGC ATC AAA ATG TAATTCTACA	1595
Leu Ser Gln Leu Ser Gln Gln Glu Gly Ile Lys Met	
495 500	
GCTTTGCCTG AACTCTCCTT TTTTCTTCAG ATCTGCTCCT GGGTTTTAAT TTGGGAGGTC	1655
AGTTGTTCTA CCTCACTGAG AGGGAACAGA AGGATATTGC TTCCTTTTGC AGCAGTGTA	1715
TAAAGTCAAT TAAAACTTC CCAGGATTTT TTTGGACCCA GGAAACAGCC ATGTGGGTCC	1775
TTTCTGTGCA CTATGAACGC TTCTTTCCCA GGACAGAAAA TGTGTAGTCT ACCTTTATTT	1835
TTTATTAACA AAACCTGTTT TTTAAAAAGA TGATTGCTGG TCTTAACTTT AGGTAACCTT	1895
GCTGTGCTGG AGATCATCTT TAAGGGCAAA GGAGTTGGAT TGCTGAATTA CAATGAAACA	1955
TGTCTTATTA CTAAAGAAAG TGATTTACTC CTGGTTAGTA CATTCTCAGA GGATTCTGAA	2015
CCACTAGAGT TTCCTTGATT CAGACTTTGA ATGTACTGTT CTATAGTTTT TCAGGATCTT	2075
AAAATAACA CTTATAAAC TCTTATCTTG AGTCTAAAAA TGACCTCATA TAGTAGTGAG	2135
GAACATAATT CATGCAATTG TATTTTGTAT ACTATTATTG TTCTTTCACT TATTCAGAAC	2195

ATTACATGCC TTCAAATGG GATTGTACTA TACCAGTAAG TGCCACTTCT GTGTCTTTCT 2255  
AATGGAAATG AGTAGAATTG CTGAAAGTCT CTATGTTAAA ACCTATAGTG TTT 2308

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 503 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met	Glu	Ala	Ala	Val	Ala	Ala	Pro	Arg	Pro	Arg	Leu	Leu	Leu	Leu	Val
1				5					10					15	
Leu	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Pro	Gly	Ala	Thr
			20					25					30		
Ala	Leu	Gln	Cys	Phe	Cys	His	Leu	Cys	Thr	Lys	Asp	Asn	Phe	Thr	Cys
		35					40					45			
Val	Thr	Asp	Gly	Leu	Cys	Phe	Val	Ser	Val	Thr	Glu	Thr	Thr	Asp	Lys
	50					55					60				
Val	Ile	His	Asn	Ser	Met	Cys	Ile	Ala	Glu	Ile	Asp	Leu	Ile	Pro	Arg
	65				70					75				80	
Asp	Arg	Pro	Phe	Val	Cys	Ala	Pro	Ser	Ser	Lys	Thr	Gly	Ser	Val	Thr
			85						90					95	
Thr	Thr	Tyr	Cys	Cys	Asn	Gln	Asp	His	Cys	Asn	Lys	Ile	Glu	Leu	Pro
		100					105					110			
Thr	Thr	Val	Lys	Ser	Ser	Pro	Gly	Leu	Gly	Pro	Val	Glu	Leu	Ala	Ala
		115					120					125			
Val	Ile	Ala	Gly	Pro	Val	Cys	Phe	Val	Cys	Ile	Ser	Leu	Met	Leu	Met
	130					135					140				
Val	Tyr	Ile	Cys	His	Asn	Arg	Thr	Val	Ile	His	His	Arg	Val	Pro	Asn
	145				150					155				160	
Glu	Glu	Asp	Pro	Ser	Leu	Asp	Arg	Pro	Phe	Ile	Ser	Glu	Gly	Thr	Thr
			165						170					175	
Leu	Lys	Asp	Leu	Ile	Tyr	Asp	Met	Thr	Thr	Ser	Gly	Ser	Gly	Ser	Gly
		180					185					190			
Leu	Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Arg	Thr	Ile	Val	Leu	Gln
	195					200						205			
Glu	Ser	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly	Lys	Trp
	210					215					220				
Arg	Gly	Glu	Glu	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu	Glu	Arg
	225				230				235					240	
Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu	Arg	His
			245						250					255	
Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn	Gly	Thr
		260					265					270			
Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly	Ser	Leu
	275					280						285			
Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Val	Glu	Gly	Met	Ile	Lys
	290					295					300				
Leu	Ala	Leu	Ser	Thr	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met	Glu	Ile
	305				310					315				320	
Val	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser
			325						330					335	
Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu
		340						345				350			
Gly	Leu	Ala	Val	Arg	His	Asp	Ser	Ala	Thr	Asp	Thr	Ile	Asp	Ile	Ala
		355					360					365			

Pro Asn His Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu  
 370 375 380  
 Asp Asp Ser Ile Asn Met Lys His Phe Glu Ser Phe Lys Arg Ala Asp  
 385 390 395 400  
 Ile Tyr Ala Met Gly Leu Val Phe Trp Glu Ile Ala Arg Arg Cys Ser  
 405 410 415  
 Ile Gly Gly Ile His Glu Asp Tyr Gln Leu Pro Tyr Tyr Asp Leu Val  
 420 425 430  
 Pro Ser Asp Pro Ser Val Glu Glu Met Arg Lys Val Val Cys Glu Gln  
 435 440 445  
 Lys Leu Arg Pro Asn Ile Pro Asn Arg Trp Gln Ser Cys Glu Ala Leu  
 450 455 460  
 Arg Val Met Ala Lys Ile Met Arg Glu Cys Trp Tyr Ala Asn Gly Ala  
 465 470 475 480  
 Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Ser Gln Leu Ser  
 485 490 495  
 Gln Gln Glu Gly Ile Lys Met  
 500

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1922 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 241..1746

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GAGAGCACAG CCCTTCCCAG TCCCCGGAGC CGCCGCGCCA CGCGCGCATG ATCAAGACCT	60
TTTCCCCGGC CCCACAGGGC CTCTGGACGT GAGACCCCGG CCGCCTCCGC AAGGAGAGGC	120
GGGGGTTCGAG TCGCCCTGTC CAAAGGCCTC AATCTAAACA ATCTTGATTC CTGTTGCCGG	180
CTGGCGGGAC CCTGAATGGC AGGAAATCTC ACCACATCTC TTCTCCTATC TCCAAGGACC	240
ATG ACC TTG GGG AGC TTC AGA AGG GGC CTT TTG ATG CTG TCG GTG GCC	288
Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala	
1 5 10 15	
TTG GGC CTA ACC CAG GGG AGA CTT GCG AAG CCT TCC AAG CTG GTG AAC	336
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn	
20 25 30	
TGC ACT TGT GAG AGC CCA CAC TGC AAG AGA CCA TTC TGC CAG GGG TCA	384
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser	
35 40 45	
TGG TGC ACA GTG GTG CTG GTT CGA GAG CAG GGC AGG CAC CCC CAG GTC	432
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val	
50 55 60	
TAT CGG GGC TGT GGG AGC CTG AAC CAG GAG CTC TGC TTG GGA CGT CCC	480
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro	
65 70 75 80	
ACG GAG TTT CTG AAC CAT CAC TGC TGC TAT AGA TCC TTC TGC AAC CAC	528
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His	

				85				90				95					
AAC	GTG	TCT	CTG	ATG	CTG	GAG	GCC	ACC	CAA	ACT	CCT	TCG	GAG	GAG	CCA	576	
Asn	Val	Ser	Leu	Met	Leu	Glu	Ala	Thr	Gln	Thr	Pro	Ser	Glu	Glu	Pro		
100								105				110					
GAA	GTT	GAT	GCC	CAT	CTG	CCT	CTG	ATC	CTG	GGT	CCT	GTG	CTG	GCC	TTG	624	
Glu	Val	Asp	Ala	His	Leu	Pro	Leu	Ile	Leu	Gly	Pro	Val	Leu	Ala	Leu		
115								120				125					
CCG	GTC	CTG	GTG	GCC	CTG	GGT	GCT	CTG	GGC	TTG	TGG	CGT	GTC	CGG	CGG	672	
Pro	Val	Leu	Val	Ala	Leu	Gly	Ala	Leu	Gly	Leu	Trp	Arg	Val	Arg	Arg		
130								135				140					
AGG	CAG	GAG	AAG	CAG	CGG	GAT	TTG	CAC	AGT	GAC	CTG	GGC	GAG	TCC	AGT	720	
Arg	Gln	Glu	Lys	Gln	Arg	Asp	Leu	His	Ser	Asp	Leu	Gly	Glu	Ser	Ser		
145				150				155				160					
CTC	ATC	CTG	AAG	GCA	TCT	GAA	CAG	GCA	GAC	AGC	ATG	TTG	GGG	GAC	TTC	768	
Leu	Ile	Leu	Lys	Ala	Ser	Glu	Gln	Ala	Asp	Ser	Met	Leu	Gly	Asp	Phe		
				165				170				175					
CTG	GAC	AGC	GAC	TGT	ACC	ACG	GGC	AGC	GGC	TCG	GGG	CTC	CCC	TTC	TTG	816	
Leu	Asp	Ser	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu		
180								185				190					
GTG	CAG	AGG	ACG	GTA	GCT	CGG	CAG	GTT	GCG	CTG	GTA	GAG	TGT	GTG	GGA	864	
Val	Gln	Arg	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly		
195								200				205					
AAG	GGC	CGA	TAT	GGC	GAG	GTG	TGG	CGC	GGT	TCG	TGG	CAT	GGC	GAA	AGC	912	
Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Ser	Trp	His	Gly	Glu	Ser		
210				215				220									
GTG	GCG	GTC	AAG	ATT	TTC	TCC	TCA	CGA	GAT	GAG	CAG	TCC	TGG	TTC	CGG	960	
Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg		
225				230				235				240					
GAG	ACG	GAG	ATC	TAC	AAC	ACA	GTT	CTG	CTT	AGA	CAC	GAC	AAC	ATC	CTA	1008	
Glu	Thr	Glu	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu		
245								250				255					
GGC	TTC	ATC	GCC	TCC	GAC	ATG	ACT	TCG	CGG	AAC	TCG	AGC	ACG	CAG	CTG	1056	
Gly	Phe	Ile	Ala	Ser	Asp	Met	Thr	Ser	Arg	Asn	Ser	Ser	Thr	Gln	Leu		
260				265				270									
TGG	CTC	ATC	ACC	CAC	TAC	CAT	GAA	CAC	GGC	TCC	CTC	TAT	GAC	TTT	CTG	1104	
Trp	Leu	Ile	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu		
275				280				285									
CAG	AGG	CAG	ACG	CTG	GAG	CCC	CAG	TTG	GCC	CTG	AGG	CTA	GCT	GTG	TCC	1152	
Gln	Arg	Gln	Thr	Leu	Glu	Pro	Gln	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser		
290				295				300									
CCG	GCC	TGC	GGC	CTG	GCG	CAC	CTA	CAT	GTG	GAG	ATC	TTT	GGC	ACT	CAA	1200	
Pro	Ala	Cys	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln		
305				310				315				320					
GGC	AAA	CCA	GCC	ATT	GCC	CAT	CGT	GAC	CTC	AAG	AGT	CGC	AAT	GTG	CTG	1248	
Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Arg	Asn	Val	Leu		
325				330				335									
GTC	AAG	AGT	AAC	TTG	CAG	TGT	TGC	ATT	GCA	GAC	CTG	GGA	CTG	GCT	GTG	1296	
Val	Lys	Ser	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val		
340				345				350									
ATG	CAC	TCA	CAA	AGC	AAC	GAG	TAC	CTG	GAT	ATC	GGC	AAC	ACA	CCC	CGA	1344	
Met	His	Ser	Gln	Ser	Asn	Glu	Tyr	Leu	Asp	Ile	Gly	Asn	Thr	Pro	Arg		
355				360				365									
GTG	GGT	ACC	AAA	AGA	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAT	GAG	CAC	ATC	1392	
Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	His	Ile		
370				375				380									
CGC	ACA	GAC	TGC	TTT	GAG	TCG	TAC	AAG	TGG	ACA	GAC	ATC	TGG	GCC	TTT	1440	
Arg	Thr	Asp	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe		

385		390		395		400	
GGC CTA GTG CTA TGG GAG ATC GCC CGG CGG ACC ATC ATC AAT GGC ATT							1488
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile							
	405			410		415	
GTG GAG GAT TAC AGG CCA CCT TTC TAT GAC ATG GTA CCC AAT GAC CCC							1536
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro							
	420			425		430	
AGT TTT GAG GAC ATG AAA AAG GTG GTG TGC GTT GAC CAG CAG ACA CCC							1584
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro							
	435			440		445	
ACC ATC CCT AAC CGG CTG GCT GCA GAT CCG GTC CTC TCC GGG CTG GCC							1632
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala							
	450			455		460	
CAG ATG ATG AGA GAG TGC TGG TAC CCC AAC CCC TCT GCT CGC CTC ACC							1680
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr							
	465			470		475	480
GCA CTG CGC ATA AAG AAG ACA TTG CAG AAG CTC AGT CAC AAT CCA GAG							1728
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu							
	485			490		495	
AAG CCC AAA GTG ATT CAC TAGCCCAGGG CCACCAGGCT TCCTCTGCCT							1776
Lys Pro Lys Val Ile His							
	500						
AAAGTGTGTG CTGGGGAAGA AGACATAGCC TGTCTGGGTA GAGGGAGTGA AGAGAGTGTG							1836
CACGCTGCCC TGTGTGTGCC TGCTCAGCTT GCTCCCAGCC CATCCAGCCA AAAATACAGC							1896
TGAGCTGAAA TTCAAAAAAA AAAAAA							1922

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Thr Leu Gly Ser Phe Arg Arg Gly Leu Leu Met Leu Ser Val Ala																	
1		5				10					15						
Leu Gly Leu Thr Gln Gly Arg Leu Ala Lys Pro Ser Lys Leu Val Asn																	
	20					25					30						
Cys Thr Cys Glu Ser Pro His Cys Lys Arg Pro Phe Cys Gln Gly Ser																	
	35					40					45						
Trp Cys Thr Val Val Leu Val Arg Glu Gln Gly Arg His Pro Gln Val																	
	50					55					60						
Tyr Arg Gly Cys Gly Ser Leu Asn Gln Glu Leu Cys Leu Gly Arg Pro																	
	65					70					75						80
Thr Glu Phe Leu Asn His His Cys Cys Tyr Arg Ser Phe Cys Asn His																	
		85							90								95
Asn Val Ser Leu Met Leu Glu Ala Thr Gln Thr Pro Ser Glu Glu Pro																	
	100								105								110
Glu Val Asp Ala His Leu Pro Leu Ile Leu Gly Pro Val Leu Ala Leu																	
	115								120								125
Pro Val Leu Val Ala Leu Gly Ala Leu Gly Leu Trp Arg Val Arg Arg																	
	130								135								140
Arg Gln Glu Lys Gln Arg Asp Leu His Ser Asp Leu Gly Glu Ser Ser																	
	145					150					155						160
Leu Ile Leu Lys Ala Ser Glu Gln Ala Asp Ser Met Leu Gly Asp Phe																	
		165							170								175
Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu																	

180	185	190
Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly		
195	200	205
Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Ser Trp His Gly Glu Ser		
210	215	220
Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe Arg		
225	230	235
Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile Leu		
245	250	255
Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln Leu		
260	265	270
Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe Leu		
275	280	285
Gln Arg Gln Thr Leu Glu Pro Gln Leu Ala Leu Arg Leu Ala Val Ser		
290	295	300
Pro Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr Gln		
305	310	315
Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Arg Asn Val Leu		
325	330	335
Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala Val		
340	345	350
Met His Ser Gln Ser Asn Glu Tyr Leu Asp Ile Gly Asn Thr Pro Arg		
355	360	365
Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu His Ile		
370	375	380
Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala Phe		
385	390	395
Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Ile Asn Gly Ile		
405	410	415
Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Met Val Pro Asn Asp Pro		
420	425	430
Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro		
435	440	445
Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala		
450	455	460
Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr		
465	470	475
Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Leu Ser His Asn Pro Glu		
485	490	495
Lys Pro Lys Val Ile His		
500		

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2070 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 217..1812

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATTCATGAGA	TGGAAGCATA	GGTCAAAGCT	GTTCGGAGAA	ATTGGAACTA	CAGTTTTATC	60
TAGCCACATC	TCTGAGAATT	CTGAAGAAAG	CAGCAGGTGA	AAGTCATTGC	CAAGTGATTT	120
TGTTCTGTAA	GGAAGCCTCC	CTCATTCACT	TACACCAGTG	AGACAGCAGG	ACCAGTCATT	180
CAAAGGGCCG	TGTACAGGAC	GCGTGGCAAT	CAGACA ATG	ACT CAG CTA	TAC ACT	234
			Met Thr Gln Leu Tyr Thr			
			1	5		
TAC ATC AGA TTA CTG GGA GCC TGT CTG TTC ATC ATT TCT CAT GTT CAA						282
Tyr Ile Arg Leu Leu Gly Ala Cys Leu Phe Ile Ile Ser His Val Gln						
	10		15		20	
GGG CAG AAT CTA GAT AGT ATG CTC CAT GGC ACT GGT ATG AAA TCA GAC						330
Gly Gln Asn Leu Asp Ser Met Leu His Gly Thr Gly Met Lys Ser Asp						
	25		30		35	
TTG GAC CAG AAG AAG CCA GAA AAT GGA GTG ACT TTA GCA CCA GAG GAT						378
Leu Asp Gln Lys Lys Pro Glu Asn Gly Val Thr Leu Ala Pro Glu Asp						
	40		45		50	
ACC TTG CCT TTC TTA AAG TGC TAT TGC TCA GGA CAC TGC CCA GAT GAT						426
Thr Leu Pro Phe Leu Lys Cys Tyr Cys Ser Gly His Cys Pro Asp Asp						
	55		60		65	70
GCT ATT AAT AAC ACA TGC ATA ACT AAT GGC CAT TGC TTT GCC ATT ATA						474
Ala Ile Asn Asn Thr Cys Ile Thr Asn Gly His Cys Phe Ala Ile Ile						
	75		80		85	
GAA GAA GAT GAT CAG GGA GAA ACC ACA TTA ACT TCT GGG TGT ATG AAG						522
Glu Glu Asp Asp Gln Gly Glu Thr Thr Leu Thr Ser Gly Cys Met Lys						
	90		95		100	
TAT GAA GGC TCT GAT TTT CAA TGC AAG GAT TCA CCG AAA GCC CAG CTA						570
Tyr Glu Gly Ser Asp Phe Gln Cys Lys Asp Ser Pro Lys Ala Gln Leu						
	105		110		115	
CGC AGG ACA ATA GAA TGT TGT CGG ACC AAT TTG TGC AAC CAG TAT TTG						618
Arg Arg Thr Ile Glu Cys Cys Arg Thr Asn Leu Cys Asn Gln Tyr Leu						
	120		125		130	
CAG CCT ACA CTG CCC CCT GTT GTT ATA GGT CCG TTC TTT GAT GGC AGC						666
Gln Pro Thr Leu Pro Val Val Ile Gly Pro Phe Phe Asp Gly Ser						
	135		140		145	150
ATC CGA TGG CTG GTT GTG CTC ATT TCC ATG GCT GTC TGT ATA GTT GCT						714
Ile Arg Trp Leu Val Val Leu Ile Ser Met Ala Val Cys Ile Val Ala						
	155		160		165	
ATG ATC ATC TTC TCC AGC TGC TTT TGC TAT AAG CAT TAT TGT AAG AGT						762
Met Ile Ile Phe Ser Ser Cys Phe Cys Tyr Lys His Tyr Cys Lys Ser						
	170		175		180	
ATC TCA AGC AGG GGT CGT TAC AAC CGT GAT TTG GAA CAG GAT GAA GCA						810
Ile Ser Ser Arg Gly Arg Tyr Asn Arg Asp Leu Glu Gln Asp Glu Ala						
	185		190		195	
TTT ATT CCA GTA GGA GAA TCA TTG AAA GAC CTG ATT GAC CAG TCC CAA						858
Phe Ile Pro Val Gly Glu Ser Leu Lys Asp Leu Ile Asp Gln Ser Gln						
	200		205		210	
AGC TCT GGG AGT GGA TCT GGA TTG CCT TTA TTG GTT CAG CGA ACT ATT						906
Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr Ile						
	215		220		225	230
GCC AAA CAG ATT CAG ATG GTT CGG CAG GTT GGT AAA GGC CGC TAT GGA						954
Ala Lys Gln Ile Gln Met Val Arg Gln Val Gly Lys Gly Arg Tyr Gly						
	235		240		245	
GAA GTA TGG ATG GGT AAA TGG CGT GGT GAA AAA GTG GCT GTC AAA GTG						1002
Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys Val						
	250		255		260	
TTT TTT ACC ACT GAA GAA GCT AGC TGG TTT AGA GAA ACA GAA ATC TAC						1050

Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr		
		265					270				275						
CAG	ACG	GTG	TTA	ATG	CGT	CAT	GAA	AAT	ATA	CTT	GGT	TTT	ATA	GCT	GCA	1098	
Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala		
		280					285				290						
GAC	ATT	AAA	GGC	ACT	GGT	TCC	TGG	ACT	CAG	CTG	TAT	TTG	ATT	ACT	GAT	1146	
Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp		
295					300					305					310		
TAC	CAT	GAA	AAT	GGA	TCT	CTC	TAT	GAC	TTC	CTG	AAA	TGT	GCC	ACA	CTA	1194	
Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Lys	Cys	Ala	Thr	Leu		
				315					320					325			
GAC	ACC	AGA	GCC	CTA	CTC	AAG	TTA	GCT	TAT	TCT	GCT	GCT	TGT	GGT	CTG	1242	
Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr	Ser	Ala	Ala	Cys	Gly	Leu		
			330					335					340				
TGC	CAC	CTC	CAC	ACA	GAA	ATT	TAT	GGT	ACC	CAA	GGG	AAG	CCT	GCA	ATT	1290	
Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr	Gln	Gly	Lys	Pro	Ala	Ile		
		345					350				355						
GCT	CAT	CGA	GAC	CTG	AAG	AGC	AAA	AAC	ATC	CTT	ATT	AAG	AAA	AAT	GGA	1338	
Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile	Leu	Ile	Lys	Lys	Asn	Gly		
		360				365				370							
AGT	TGC	TGT	ATT	GCT	GAC	CTG	GGC	CTA	GCT	GTT	AAA	TTC	AAC	AGT	GAT	1386	
Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Lys	Phe	Asn	Ser	Asp		
375					380				385						390		
ACA	AAT	GAA	GTT	GAC	ATA	CCC	TTG	AAT	ACC	AGG	GTG	GGC	ACC	AAG	CGG	1434	
Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg		
				395				400						405			
TAC	ATG	GCT	CCA	GAA	GTG	CTG	GAT	GAA	AGC	CTG	AAT	AAA	AAC	CAT	TTC	1482	
Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Ser	Leu	Asn	Lys	Asn	His	Phe		
			410					415					420				
CAG	CCC	TAC	ATC	ATG	GCT	GAC	ATC	TAT	AGC	TTT	GGT	TTG	ATC	ATT	TGG	1530	
Gln	Pro	Tyr	Ile	Met	Ala	Asp	Ile	Tyr	Ser	Phe	Gly	Leu	Ile	Ile	Trp		
		425					430					435					
GAA	ATG	GCT	CGT	CGT	TGT	ATT	ACA	GGA	GGA	ATC	GTG	GAG	GAA	TAT	CAA	1578	
Glu	Met	Ala	Arg	Arg	Cys	Ile	Thr	Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln		
		440				445					450						
TTA	CCA	TAT	TAC	AAC	ATG	GTG	CCC	AGT	GAC	CCA	TCC	TAT	GAG	GAC	ATG	1626	
Leu	Pro	Tyr	Tyr	Asn	Met	Val	Pro	Ser	Asp	Pro	Ser	Tyr	Glu	Asp	Met		
455					460					465					470		
CGT	GAG	GTT	GTG	TGT	GTG	AAA	CGC	TTG	CGG	CCA	ATC	GTG	TCT	AAC	CGC	1674	
Arg	Glu	Val	Val	Cys	Val	Lys	Arg	Leu	Arg	Pro	Ile	Val	Ser	Asn	Arg		
				475					480					485			
TGG	AAC	AGC	GAT	GAA	TGT	CTT	CGA	GCA	GTT	TTG	AAG	CTA	ATG	TCA	GAA	1722	
Trp	Asn	Ser	Asp	Glu	Cys	Leu	Arg	Ala	Val	Leu	Lys	Leu	Met	Ser	Glu		
			490					495					500				
TGT	TGG	GCC	CAT	AAT	CCA	GCC	TCC	AGA	CTC	ACA	GCT	TTG	AGA	ATC	AAG	1770	
Cys	Trp	Ala	His	Asn	Pro	Ala	Ser	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys		
		505					510					515					
AAG	ACA	CTT	GCA	AAA	ATG	GTT	GAA	TCC	CAG	GAT	GTA	AAG	ATT			1812	
Lys	Thr	Leu	Ala	Lys	Met	Val	Glu	Ser	Gln	Asp	Val	Lys	Ile				
		520				525					530						
TGACAATTAA	ACAATTTTGA	GGGAGAATTT	AGACTGCAAG	AACTTCTTCA	CCCAAGGAAT											1872	
GGGTGGGATT	AGCATGGAAT	AGGATGTTGA	CTTGGTTTCC	AGACTCCTTC	CTCTACATCT											1932	
TCACAGGCTG	CTAACAGTAA	ACCTTACCGT	ACTCTACAGA	ATACAAGATT	GGAAGTTGGA											1992	
ACTTCAAACA	TGTCATTCTT	TATATATGAC	AGCTTTGTTT	TAATGTGGGG	TTTTTTTGT											2052	
TGCTTTTTTT	GTTTTGTT															2070	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Thr	Gln	Leu	Tyr	Thr	Tyr	Ile	Arg	Leu	Leu	Gly	Ala	Cys	Leu	Phe
1				5					10					15	
Ile	Ile	Ser	His	Val	Gln	Gly	Gln	Asn	Leu	Asp	Ser	Met	Leu	His	Gly
			20					25					30		
Thr	Gly	Met	Lys	Ser	Asp	Leu	Asp	Gln	Lys	Lys	Pro	Glu	Asn	Gly	Val
		35					40					45			
Thr	Leu	Ala	Pro	Glu	Asp	Thr	Leu	Pro	Phe	Leu	Lys	Cys	Tyr	Cys	Ser
	50				55						60				
Gly	His	Cys	Pro	Asp	Asp	Ala	Ile	Asn	Asn	Thr	Cys	Ile	Thr	Asn	Gly
65				70				75						80	
His	Cys	Phe	Ala	Ile	Glu	Glu	Asp	Asp	Gln	Gly	Glu	Thr	Thr	Leu	
			85					90					95		
Thr	Ser	Gly	Cys	Met	Lys	Tyr	Glu	Gly	Ser	Asp	Phe	Gln	Cys	Lys	Asp
		100						105					110		
Ser	Pro	Lys	Ala	Gln	Leu	Arg	Arg	Thr	Ile	Glu	Cys	Cys	Arg	Thr	Asn
		115				120						125			
Leu	Cys	Asn	Gln	Tyr	Leu	Gln	Pro	Thr	Leu	Pro	Pro	Val	Val	Ile	Gly
	130					135					140				
Pro	Phe	Phe	Asp	Gly	Ser	Ile	Arg	Trp	Leu	Val	Val	Leu	Ile	Ser	Met
145				150					155					160	
Ala	Val	Cys	Ile	Val	Ala	Met	Ile	Ile	Phe	Ser	Ser	Cys	Phe	Cys	Tyr
			165						170					175	
Lys	His	Tyr	Cys	Lys	Ser	Ile	Ser	Ser	Arg	Gly	Arg	Tyr	Asn	Arg	Asp
		180						185					190		
Leu	Glu	Gln	Asp	Glu	Ala	Phe	Ile	Pro	Val	Gly	Glu	Ser	Leu	Lys	Asp
	195					200						205			
Leu	Ile	Asp	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Leu
	210				215						220				
Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Arg	Gln	Val
225				230						235				240	
Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg	Gly	Glu
		245						250					255		
Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser	Trp	Phe
		260					265						270		
Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu	Asn	Ile
	275					280						285			
Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp	Thr	Gln
	290				295						300				
Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr	Asp	Phe
305				310						315				320	
Leu	Lys	Cys	Ala	Thr	Leu	Asp	Thr	Arg	Ala	Leu	Leu	Lys	Leu	Ala	Tyr
			325					330						335	
Ser	Ala	Ala	Cys	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Tyr	Gly	Thr
		340					345						350		
Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys	Asn	Ile
	355					360						365			
Leu	Ile	Lys	Lys	Asn	Gly	Ser	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala
	370				375					380					
Val	Lys	Phe	Asn	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Leu	Asn	Thr
385				390						395					400

Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Ser  
 405 410 415  
 Leu Asn Lys Asn His Phe Gln Pro Tyr Ile Met Ala Asp Ile Tyr Ser  
 420 425 430  
 Phe Gly Leu Ile Ile Trp Glu Met Ala Arg Arg Cys Ile Thr Gly Gly  
 435 440 445  
 Ile Val Glu Glu Tyr Gln Leu Pro Tyr Tyr Asn Met Val Pro Ser Asp  
 450 455 460  
 Pro Ser Tyr Glu Asp Met Arg Glu Val Val Cys Val Lys Arg Leu Arg  
 465 470 475 480  
 Pro Ile Val Ser Asn Arg Trp Asn Ser Asp Glu Cys Leu Arg Ala Val  
 485 490 495  
 Leu Lys Leu Met Ser Glu Cys Trp Ala His Asn Pro Ala Ser Arg Leu  
 500 505 510  
 Thr Ala Leu Arg Ile Lys Lys Thr Leu Ala Lys Met Val Glu Ser Gln  
 515 520 525  
 Asp Val Lys Ile  
 530

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mouse

(ix) FEATURE:

- (A) NAME/KEY: CDS

- (B) LOCATION: 10..1524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CGCGGTTAC ATG GCG GAG TCG GCC GGA GCC TCC TCC TTC TTC CCC CTT	48
Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu	
1 5 10	
GTT GTC CTC CTG CTC GCC GGC AGC GGC GGG TCC GGG CCC CGG GGG ATC	96
Val Val Leu Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile	
15 20 25	
CAG GCT CTG CTG TGT GCG TGC ACC AGC TGC CTA CAG ACC AAC TAC ACC	144
Gln Ala Leu Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr	
30 35 40 45	
TGT GAG ACA GAT GGG GCT TGC ATG GTC TCC ATC TTT AAC CTG GAT GGC	192
Cys Glu Thr Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly	
50 55 60	
GTG GAG CAC CAT GTA CGT ACC TGC ATC CCC AAG GTG GAG CTG GTT CCT	240
Val Glu His His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro	
65 70 75	
GCT GGA AAG CCC TTC TAC TGC CTG AGT TCA GAG GAT CTG CGC AAC ACA	288
Ala Gly Lys Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr	
80 85 90	
CAC TGC TGC TAT ATT GAC TTC TGC AAC AAG ATT GAC CTC AGG GTC CCC	336
His Cys Cys Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro	
95 100 105	

AGC GGA CAC CTC AAG GAG CCT GCG CAC CCC TCC ATG TGG GGC CCT GTG	384
Ser Gly His Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val	
110 115 120 125	
GAG CTG GTC GGC ATC ATC GCC GGC CCC GTC TTC CTC CTC TTC CTT ATC	432
Glu Leu Val Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile	
130 135 140	
ATT ATC ATC GTC TTC CTG GTC ATC AAC TAT CAC CAG CGT GTC TAC CAT	480
Ile Ile Ile Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His	
145 150 155	
AAC CGC CAG AGG TTG GAC ATG GAG GAC CCC TCT TGC GAG ATG TGT CTC	528
Asn Arg Gln Arg Leu Asp Met Glu Asp Pro Ser Cys Glu Met Cys Leu	
160 165 170	
TCC AAA GAC AAG ACG CTC CAG GAT CTC GTC TAC GAC CTC TCC ACG TCA	576
Ser Lys Asp Lys Thr Leu Gln Asp Leu Val Tyr Asp Leu Ser Thr Ser	
175 180 185	
GGG TCT GGC TCA GGG TTA CCC CTT TTT GTC CAG CGC ACA GTG GCC CGA	624
Gly Ser Gly Ser Gly Leu Pro Leu Phe Val Gln Arg Thr Val Ala Arg	
190 195 200 205	
ACC ATT GTT TTA CAA GAG ATT ATC GGC AAG GGC CGG TTC GGG GAA GTA	672
Thr Ile Val Leu Gln Glu Ile Ile Gly Lys Gly Arg Phe Gly Glu Val	
210 215 220	
TGG CGT GGT CGC TGG AGG GGT GGT GAC GTG GCT GTG AAA ATC TTC TCT	720
Trp Arg Gly Arg Trp Arg Gly Gly Asp Val Ala Val Lys Ile Phe Ser	
225 230 235	
TCT CGT GAA GAA CGG TCT TGG TTC CGT GAA GCA GAG ATC TAC CAG ACC	768
Ser Arg Glu Glu Arg Ser Trp Phe Arg Glu Ala Glu Ile Tyr Gln Thr	
240 245 250	
GTC ATG CTG CGC CAT GAA AAC ATC CTT GGC TTT ATT GCT GCT GAC AAT	816
Val Met Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Asn	
255 260 265	
AAA GAT AAT GGC ACC TGG ACC CAG CTG TGG CTT GTC TCT GAC TAT CAC	864
Lys Asp Asn Gly Thr Trp Thr Gln Leu Trp Leu Val Ser Asp Tyr His	
270 275 280 285	
GAG CAT GGC TCA CTG TTT GAT TAT CTG AAC CGC TAC ACA GTG ACC ATT	912
Glu His Gly Ser Leu Phe Asp Tyr Leu Asn Arg Tyr Thr Val Thr Ile	
290 295 300	
GAG GGA ATG ATT AAG CTA GCC TTG TCT GCA GCC AGT GGT TTG GCA CAC	960
Glu Gly Met Ile Lys Leu Ala Leu Ser Ala Ala Ser Gly Leu Ala His	
305 310 315	
CTG CAT ATG GAG ATT GTG GGC ACT CAA GGG AAG CCG GGA ATT GCT CAT	1008
Leu His Met Glu Ile Val Gly Thr Gln Gly Lys Pro Gly Ile Ala His	
320 325 330	
CGA GAC TTG AAG TCA AAG AAC ATC CTG GTG AAA AAA AAT GGC ATG TGT	1056
Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Met Cys	
335 340 345	
GCC ATT GCA GAC CTG GGC CTG GCT GTC CGT CAT GAT GCG GTC ACT GAC	1104
Ala Ile Ala Asp Leu Gly Leu Ala Val Arg His Asp Ala Val Thr Asp	
350 355 360 365	
ACC ATA GAC ATT GCT CCA AAT CAG AGG GTG GGG ACC AAA CGA TAC ATG	1152
Thr Ile Asp Ile Ala Pro Asn Gln Arg Val Gly Thr Lys Arg Tyr Met	
370 375 380	
GCT CCT GAA GTC CTT GAC GAG ACA ATC AAC ATG AAG CAC TTT GAC TCC	1200
Ala Pro Glu Val Leu Asp Glu Thr Ile Asn Met Lys His Phe Asp Ser	
385 390 395	
TTC AAA TGT GCC GAC ATC TAT GCC CTC GGG CTT GTC TAC TGG GAG ATT	1248
Phe Lys Cys Ala Asp Ile Tyr Ala Leu Gly Leu Val Tyr Trp Glu Ile	
400 405 410	

GCA CGA AGA TGC AAT TCT GGA GGA GTC CAT GAA GAC TAT CAA CTG CCG	1296
Ala Arg Arg Cys Asn Ser Gly Gly Val His Glu Asp Tyr Gln Leu Pro	
415 420 425	
TAT TAC GAC TTA GTG CCC TCC GAC CCT TCC ATT GAG GAG ATG CGA AAG	1344
Tyr Tyr Asp Leu Val Pro Ser Asp Pro Ser Ile Glu Glu Met Arg Lys	
430 435 440 445	
GTT GTA TGT GAC CAG AAG CTA CGG CCC AAT GTC CCC AAC TGG TGG CAG	1392
Val Val Cys Asp Gln Lys Leu Arg Pro Asn Val Pro Asn Trp Trp Gln	
450 455 460	
AGT TAT GAG GCC TTG CGA GTG ATG GGA AAG ATG ATG CGG GAG TGC TGG	1440
Ser Tyr Glu Ala Leu Arg Val Met Gly Lys Met Met Arg Glu Cys Trp	
465 470 475	
TAC GCC AAT GGT GCT GCC CGT CTG ACA GCT CTG CGC ATC AAG AAG ACT	1488
Tyr Ala Asn Gly Ala Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr	
480 485 490	
CTG TCC CAG CTA AGC GTG CAG GAA GAT GTG AAG ATT TAAGCTGTTC	1534
Leu Ser Gln Leu Ser Val Gln Glu Asp Val Lys Ile	
495 500 505	
CTCTGCCTAC ACAAAGAACC TGGGCAGTGA GGATGACTGC AGCCACCGTG CAAGCGTCGT	1594
GGAGGCCTAT CCTCTTGTTT CTGCCCCGCC CTCTGGCAGA GCCCTGGCCT GCAAGAGGGA	1654
CAGAGCCTGG GAGACGCGCG CACTCCCGTT GGGTTTGAGA CAGACACTTT TTATATTTAC	1714
CTCCTGATGG CATGGAGACC TGAGCAAATC ATGTAGTCAC TCAATGCCAC AACTCAAAC	1774
GCTTCAGTGG GAAGTACAGA GACCCAGTGC ATTGCGTGTG CAGGAGCGTG AGGTGCTGGG	1834
CTCGCCAGGA GCGGCCCCCA TACCTTGTGG TCCACTGGGC TGCAGGTTTT CCTCCAGGGA	1894
CCAGTCAACT GGCATCAAGA TATTGAGAGG AACCGGAAGT TTCTCCCTCC TTCCCGTAGC	1954
AGTCCTGAGC CACACCATCC TTCTCATGGA CATCCGGAGG ACTGCCCCCTA GAGACACAAC	2014
CTGCTGCCTG TCTGTCCAGC CAAGTGCGCA TGTGCCGAGG TGTGTCCCAC ATTGTGCCTG	2074
GTCTGTGCCA CGCCCGTGTG TGTGTGTGTG TGTGTGAGTG AGTGTGTGTG TGTACTTA	2134
ACCTGCTTGA GCTTCTGTGC ATGTGT	2160

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 505 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Ala Glu Ser Ala Gly Ala Ser Ser Phe Phe Pro Leu Val Val Leu	
1 5 10 15	
Leu Leu Ala Gly Ser Gly Gly Ser Gly Pro Arg Gly Ile Gln Ala Leu	
20 25 30	
Leu Cys Ala Cys Thr Ser Cys Leu Gln Thr Asn Tyr Thr Cys Glu Thr	
35 40 45	
Asp Gly Ala Cys Met Val Ser Ile Phe Asn Leu Asp Gly Val Glu His	
50 55 60	
His Val Arg Thr Cys Ile Pro Lys Val Glu Leu Val Pro Ala Gly Lys	
65 70 75 80	
Pro Phe Tyr Cys Leu Ser Ser Glu Asp Leu Arg Asn Thr His Cys Cys	
85 90 95	
Tyr Ile Asp Phe Cys Asn Lys Ile Asp Leu Arg Val Pro Ser Gly His	
100 105 110	
Leu Lys Glu Pro Ala His Pro Ser Met Trp Gly Pro Val Glu Leu Val	
115 120 125	
Gly Ile Ile Ala Gly Pro Val Phe Leu Leu Phe Leu Ile Ile Ile Ile	
130 135 140	
Val Phe Leu Val Ile Asn Tyr His Gln Arg Val Tyr His Asn Arg Gln	

145		150		155		160									
Arg	Leu	Asp	Met	Glu	Asp	Pro	Ser	Cys	Glu	Met	Cys	Leu	Ser	Lys	Asp
		165							170					175	
Lys	Thr	Leu	Gln	Asp	Leu	Val	Tyr	Asp	Leu	Ser	Thr	Ser	Gly	Ser	Gly
		180						185					190		
Ser	Gly	Leu	Pro	Leu	Phe	Val	Gln	Arg	Thr	Val	Ala	Arg	Thr	Ile	Val
		195						200				205			
Leu	Gln	Glu	Ile	Ile	Gly	Lys	Gly	Arg	Phe	Gly	Glu	Val	Trp	Arg	Gly
		210						215			220				
Arg	Trp	Arg	Gly	Gly	Asp	Val	Ala	Val	Lys	Ile	Phe	Ser	Ser	Arg	Glu
225					230					235					240
Glu	Arg	Ser	Trp	Phe	Arg	Glu	Ala	Glu	Ile	Tyr	Gln	Thr	Val	Met	Leu
				245					250					255	
Arg	His	Glu	Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Asn	Lys	Asp	Asn
			260					265					270		
Gly	Thr	Trp	Thr	Gln	Leu	Trp	Leu	Val	Ser	Asp	Tyr	His	Glu	His	Gly
		275						280				285			
Ser	Leu	Phe	Asp	Tyr	Leu	Asn	Arg	Tyr	Thr	Val	Thr	Ile	Glu	Gly	Met
		290				295					300				
Ile	Lys	Leu	Ala	Leu	Ser	Ala	Ala	Ser	Gly	Leu	Ala	His	Leu	His	Met
305					310					315					320
Glu	Ile	Val	Gly	Thr	Gln	Gly	Lys	Pro	Gly	Ile	Ala	His	Arg	Asp	Leu
				325					330					335	
Lys	Ser	Lys	Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Met	Cys	Ala	Ile	Ala
			340					345				350			
Asp	Leu	Gly	Leu	Ala	Val	Arg	His	Asp	Ala	Val	Thr	Asp	Thr	Ile	Asp
		355						360				365			
Ile	Ala	Pro	Asn	Gln	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Ala	Pro	Glu
		370				375					380				
Val	Leu	Asp	Glu	Thr	Ile	Asn	Met	Lys	His	Phe	Asp	Ser	Phe	Lys	Cys
385					390					395					400
Ala	Asp	Ile	Tyr	Ala	Leu	Gly	Leu	Val	Tyr	Trp	Glu	Ile	Ala	Arg	Arg
				405					410					415	
Cys	Asn	Ser	Gly	Gly	Val	His	Glu	Asp	Tyr	Gln	Leu	Pro	Tyr	Tyr	Asp
			420					425					430		
Leu	Val	Pro	Ser	Asp	Pro	Ser	Ile	Glu	Glu	Met	Arg	Lys	Val	Val	Cys
		435						440				445			
Asp	Gln	Lys	Leu	Arg	Pro	Asn	Val	Pro	Asn	Trp	Trp	Gln	Ser	Tyr	Glu
		450				455					460				
Ala	Leu	Arg	Val	Met	Gly	Lys	Met	Met	Arg	Glu	Cys	Trp	Tyr	Ala	Asn
465					470					475					480
Gly	Ala	Ala	Arg	Leu	Thr	Ala	Leu	Arg	Ile	Lys	Lys	Thr	Leu	Ser	Gln
				485				490						495	
Leu	Ser	Val	Gln	Glu	Asp	Val	Lys	Ile							
			500					505							

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1952 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mouse

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..1692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AAGCGGCGGC AGAAGTTGCC GGC GTGGTGC TCGTAGTGAG GGCGCGGAGG ACCCGGGGACC	60
TGGGAAGCGG CGGCGGGTTA ACTTCGGCTG AATCACAACC ATTTGGCGCT GAGCTATGAC	120
AAGAGAGCAA ACAAAAAGTT AAAGGAGCAA CCCGGCCATA AGTGAAGAGA GAAGTTTATT	180
GATAAC ATG CTC TTA CGA AGC TCT GGA AAA TTA AAT GTG GGC ACC AAG	228
Met Leu Leu Arg Ser Ser Gly Lys Leu Asn Val Gly Thr Lys	
1 5 10	
AAG GAG GAT GGA GAG AGT ACA GCC CCC ACC CCT CGG CCC AAG ATC CTA	276
Lys Glu Asp Gly Glu Ser Thr Ala Pro Thr Pro Arg Pro Lys Ile Leu	
15 20 25 30	
CGT TGT AAA TGC CAC CAC CAC TGT CCG GAA GAC TCA GTC AAC AAT ATC	324
Arg Cys Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile	
35 40 45	
TGC AGC ACA GAT GGG TAC TGC TTC ACG ATG ATA GAA GAA GAT GAC TCT	372
Cys Ser Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser	
50 55 60	
GGA ATG CCT GTT GTC ACC TCT GGA TGT CTA GGA CTA GAA GGG TCA GAT	420
Gly Met Pro Val Val Thr Ser Gly Cys Leu Gly Leu Glu Gly Ser Asp	
65 70 75	
TTT CAA TGT CGT GAC ACT CCC ATT CCT CAT CAA AGA AGA TCA ATT GAA	468
Phe Gln Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu	
80 85 90	
TGC TGC ACA GAA AGG AAT GAG TGT AAT AAA GAC CTC CAC CCC ACT CTG	516
Cys Cys Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu	
95 100 105 110	
CCT CCT CTC AAG GAC AGA GAT TTT GTT GAT GGG CCC ATA CAC CAC AAG	564
Pro Pro Leu Lys Asp Arg Asp Phe Val Asp Gly Pro Ile His His Lys	
115 120 125	
GCC TTG CTT ATC TCT GTG ACT GTC TGT AGT TTA CTC TTG GTC CTC ATT	612
Ala Leu Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile	
130 135 140	
ATT TTA TTC TGT TAC TTC AGG TAT AAA AGA CAA GAA GCC CGA CCT CGG	660
Ile Leu Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Ala Arg Pro Arg	
145 150 155	
TAC AGC ATT GGG CTG GAG CAG GAC GAG ACA TAC ATT CCT CCT GGA GAG	708
Tyr Ser Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu	
160 165 170	
TCC CTG AGA GAC TTG ATC GAG CAG TCT CAG AGC TCG GGA AGT GGA TCA	756
Ser Leu Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser	
175 180 185 190	
GGC CTC CCT CTG CTG GTC CAA AGG ACA ATA GCT AAG CAA ATT CAG ATG	804
Gly Leu Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met	
195 200 205	
GTG AAG CAG ATT GGA AAA GGC CGC TAT GGC GAG GTG TGG ATG GGA AAG	852
Val Lys Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys	
210 215 220	
TGG CGT GGA GAA AAG GTG GCT GTG AAA GTG TTC TTC ACC ACG GAG GAA	900
Trp Arg Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu	
225 230 235	
GCC AGC TGG TTC CGA GAG ACT GAG ATA TAT CAG ACG GTC CTG ATG CGG	948
Ala Ser Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg	
240 245 250	

CAT GAG AAT ATT CTG GGG TTC ATT GCT GCA GAT ATC AAA GGG ACT GGG	996
His Glu Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly	
255 260 265 270	
TCC TGG ACT CAG TTG TAC CTC ATC ACA GAC TAT CAT GAA AAC GGC TCC	1044
Ser Trp Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser	
275 280 285	
CTT TAT GAC TAT CTG AAA TCC ACC ACC TTA GAC GCA AAG TCC ATG CTG	1092
Leu Tyr Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu	
290 295 300	
AAG CTA GCC TAC TCC TCT GTC AGC GGC CTA TGC CAT TTA CAC ACG GAA	1140
Lys Leu Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu	
305 310 315	
ATC TTT AGC ACT CAA GGC AAG CCA GCA ATC GCC CAT CGA GAC TTG AAA	1188
Ile Phe Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys	
320 325 330	
AGT AAA AAC ATC CTG GTG AAG AAA AAT GGA ACT TGC TGC ATA GCA GAC	1236
Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp	
335 340 345 350	
CTG GGC TTG GCT GTC AAG TTC ATT AGT GAC ACA AAT GAG GTT GAC ATC	1284
Leu Gly Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile	
355 360 365	
CCA CCC AAC ACC CGG GTT GGC ACC AAG CGC TAT ATG CCT CCA GAA GTG	1332
Pro Pro Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val	
370 375 380	
CTG GAC GAG AGC TTG AAT AGA AAC CAT TTC CAG TCC TAC ATT ATG GCT	1380
Leu Asp Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala	
385 390 395	
GAC ATG TAC AGC TTT GGA CTC ATC CTC TGG GAG ATT GCA AGG AGA TGT	1428
Asp Met Tyr Ser Phe Gly Leu Ile Leu Trp Glu Ile Ala Arg Arg Cys	
400 405 410	
GTT TCT GGA GGT ATA GTG GAA GAA TAC CAG CTT CCC TAT CAC GAC CTG	1476
Val Ser Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu	
415 420 425 430	
GTG CCC AGT GAC CCT TCT TAT GAG GAC ATG AGA GAA ATT GTG TGC ATG	1524
Val Pro Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Met	
435 440 445	
AAG AAG TTA CGG CCT TCA TTC CCC AAT CGA TGG AGC AGT GAT GAG TGT	1572
Lys Lys Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys	
450 455 460	
CTC AGG CAG ATG GGG AAG CTT ATG ACA GAG TGC TGG GCG CAG AAT CCT	1620
Leu Arg Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala Gln Asn Pro	
465 470 475	
GCC TCC AGG CTG ACG GCC CTG AGA GTT AAG AAA ACC CTT GCC AAA ATG	1668
Ala Ser Arg Leu Thr Ala Leu Arg Val Lys Lys Thr Leu Ala Lys Met	
480 485 490	
TCA GAG TCC CAG GAC ATT AAA CTC TGACGTCAGA TACTTGTGGA CAGAGCAAGA	1722
Ser Glu Ser Gln Asp Ile Lys Leu	
495 500	
ATTTACACAGA AGCATCGTTA GCCCAAGCCT TGAACGTTAG CCTACTGCCC AGTGAGTTCA	1782
GACTTTCCTG GAAGAGAGCA CGGTGGGCAG ACACAGAGGA ACCCAGAAAC ACGGATTCAT	1842
CATGGCTTTC TGAGGAGGAG AAACGTGTTTGG GGTAACCTTGT TCAAGATATG ATGCATGTTG	1902
CTTTCTAAGA AAGCCCTGTA TTTTGAATTA CCATTTTTTTT ATAAAAAAAAA	1952

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 502 amino acids

(B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Leu	Leu	Arg	Ser	Ser	Gly	Lys	Leu	Asn	Val	Gly	Thr	Lys	Lys	Glu
1				5				10						15	
Asp	Gly	Glu	Ser	Thr	Ala	Pro	Thr	Pro	Arg	Pro	Lys	Ile	Leu	Arg	Cys
			20					25					30		
Lys	Cys	His	His	His	Cys	Pro	Glu	Asp	Ser	Val	Asn	Asn	Ile	Cys	Ser
		35					40				45				
Thr	Asp	Gly	Tyr	Cys	Phe	Thr	Met	Ile	Glu	Glu	Asp	Asp	Ser	Gly	Met
	50					55					60				
Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln
65					70			75							80
Cys	Arg	Asp	Thr	Pro	Ile	Pro	His	Gln	Arg	Arg	Ser	Ile	Glu	Cys	Cys
			85					90						95	
Thr	Glu	Arg	Asn	Glu	Cys	Asn	Lys	Asp	Leu	His	Pro	Thr	Leu	Pro	Pro
			100					105					110		
Leu	Lys	Asp	Arg	Asp	Phe	Val	Asp	Gly	Pro	Ile	His	His	Lys	Ala	Leu
		115					120					125			
Leu	Ile	Ser	Val	Thr	Val	Cys	Ser	Leu	Leu	Leu	Val	Leu	Ile	Ile	Leu
		130				135					140				
Phe	Cys	Tyr	Phe	Arg	Tyr	Lys	Arg	Gln	Glu	Ala	Arg	Pro	Arg	Tyr	Ser
145					150				155						160
Ile	Gly	Leu	Glu	Gln	Asp	Glu	Thr	Tyr	Ile	Pro	Pro	Gly	Glu	Ser	Leu
				165				170						175	
Arg	Asp	Leu	Ile	Glu	Gln	Ser	Gln	Ser	Ser	Gly	Ser	Gly	Ser	Gly	Leu
			180					185				190			
Pro	Leu	Leu	Val	Gln	Arg	Thr	Ile	Ala	Lys	Gln	Ile	Gln	Met	Val	Lys
		195					200					205			
Gln	Ile	Gly	Lys	Gly	Arg	Tyr	Gly	Glu	Val	Trp	Met	Gly	Lys	Trp	Arg
	210				215						220				
Gly	Glu	Lys	Val	Ala	Val	Lys	Val	Phe	Phe	Thr	Thr	Glu	Glu	Ala	Ser
225					230				235						240
Trp	Phe	Arg	Glu	Thr	Glu	Ile	Tyr	Gln	Thr	Val	Leu	Met	Arg	His	Glu
			245					250						255	
Asn	Ile	Leu	Gly	Phe	Ile	Ala	Ala	Asp	Ile	Lys	Gly	Thr	Gly	Ser	Trp
		260						265					270		
Thr	Gln	Leu	Tyr	Leu	Ile	Thr	Asp	Tyr	His	Glu	Asn	Gly	Ser	Leu	Tyr
		275					280					285			
Asp	Tyr	Leu	Lys	Ser	Thr	Thr	Leu	Asp	Ala	Lys	Ser	Met	Leu	Lys	Leu
	290					295					300				
Ala	Tyr	Ser	Ser	Val	Ser	Gly	Leu	Cys	His	Leu	His	Thr	Glu	Ile	Phe
305					310					315					320
Ser	Thr	Gln	Gly	Lys	Pro	Ala	Ile	Ala	His	Arg	Asp	Leu	Lys	Ser	Lys
				325					330					335	
Asn	Ile	Leu	Val	Lys	Lys	Asn	Gly	Thr	Cys	Cys	Ile	Ala	Asp	Leu	Gly
		340						345				350			
Leu	Ala	Val	Lys	Phe	Ile	Ser	Asp	Thr	Asn	Glu	Val	Asp	Ile	Pro	Pro
		355					360					365			
Asn	Thr	Arg	Val	Gly	Thr	Lys	Arg	Tyr	Met	Pro	Pro	Glu	Val	Leu	Asp
	370					375						380			
Glu	Ser	Leu	Asn	Arg	Asn	His	Phe	Gln	Ser	Tyr	Ile	Met	Ala	Asp	Met
385					390					395					400
Tyr	Ser	Phe	Gly	Leu	Ile	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Cys	Val	Ser
				405					410					415	
Gly	Gly	Ile	Val	Glu	Glu	Tyr	Gln	Leu	Pro	Tyr	His	Asp	Leu	Val	Pro



(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: YES  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
CGGAATTCTG GTGCCATATA 20

(2) INFORMATION FOR SEQ ID NO: 23:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
ATTCAAGGGC ACATCAACTT CATTTGTGTC ACTGTTG 37

(2) INFORMATION FOR SEQ ID NO: 24:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
GCGGATCCAC CATGGCGGAG TCGGCC 26

(2) INFORMATION FOR SEQ ID NO: 25:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iii) ANTI-SENSE: NO  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
AACACCGGGC CGGCGATGAT 20

(2) INFORMATION FOR SEQ ID NO: 26:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
Gly Xaa Gly Xaa Xaa Gly  
1 5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
 Asp Phe Lys Ser Arg Asn  
 1 5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:  
 Asp Leu Lys Ser Lys Asn  
 1 5

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
 Gly Thr Lys Arg Tyr Met  
 1 5

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(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 513 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
Met Gly Ala Ala Ala Lys Leu Ala Phe Ala Val Phe Leu Ile Ser Cys
      5                               10                   15
Ser Ser Gly Ala Ile Leu Gly Arg Ser Glu Thr Gln Glu Cys Leu Phe
      20                               25                   30
Phe Asn Ala Asn Trp Glu Lys Asp Arg Thr Asn Gln Thr Gly Val Glu
      35                               40                   45
Pro Cys Tyr Gly Asp Lys Asp Lys Arg Arg His Cys Phe Ala Thr Trp
      50                               55                   60
Lys Asn Ile Ser Gly Ser Ile Glu Ile Val Lys Gln Gly Cys Trp Leu
      65                               70                   75                   80
Asp Asp Ile Asn Cys Tyr Asp Arg Thr Asp Cys Val Glu Lys Lys Asp
      85                               90                   95
Ser Pro Glu Val Tyr Phe Cys Cys Cys Glu Gly Asn Met Cys Asn Glu
      100                              105                  110
Lys Phe Ser Tyr Phe Pro Glu Met Glu Val Thr Gln Pro Thr Ser Asn

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	115					120				125					
Pro	Val	Thr	Pro	Lys	Pro	Pro	Tyr	Tyr	Asn	Ile	Leu	Leu	Tyr	Ser	Leu
	130					135					140				
Val	Pro	Leu	Met	Leu	Ile	Ala	Gly	Ile	Val	Ile	Cys	Ala	Phe	Trp	Val
145					150					155					160
Tyr	Arg	His	His	Lys	Met	Ala	Tyr	Pro	Pro	Val	Leu	Val	Pro	Thr	Gln
				165					170					175	
Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu	Leu	Gly	Leu	Lys	Pro	Leu
			180					185					190		
Gln	Leu	Leu	Glu	Val	Lys	Ala	Arg	Gly	Arg	Phe	Gly	Cys	Val	Trp	Lys
	195					200						205			
Ala	Gln	Leu	Leu	Asn	Glu	Tyr	Val	Ala	Val	Lys	Ile	Phe	Pro	Ile	Gln
210					215						220				
Asp	Lys	Gln	Ser	Trp	Gln	Asn	Glu	Tyr	Glu	Val	Tyr	Ser	Leu	Pro	Gly
225					230					235					240
Met	Lys	His	Glu	Asn	Ile	Leu	Gln	Phe	Ile	Gly	Ala	Glu	Lys	Arg	Gly
				245					250					255	
Thr	Ser	Val	Asp	Val	Asp	Leu	Trp	Leu	Ile	Thr	Ala	Phe	His	Glu	Lys
			260					265					270		
Gly	Ser	Leu	Ser	Asp	Phe	Leu	Lys	Ala	Asn	Val	Val	Ser	Trp	Asn	Glu
	275					280						285			
Leu	Cys	His	Ile	Ala	Glu	Thr	Met	Ala	Arg	Gly	Leu	Ala	Tyr	Leu	His
290					295						300				
Glu	Asp	Ile	Pro	Gly	Leu	Lys	Asp	Gly	His	Lys	Pro	Ala	Ile	Ser	His
305					310					315					320
Arg	Asp	Ile	Lys	Ser	Lys	Asn	Val	Leu	Leu	Lys	Asn	Asn	Leu	Thr	Ala
				325					330					335	
Cys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Leu	Lys	Phe	Glu	Ala	Gly	Lys	Ser
			340					345					350		
Ala	Gly	Asp	Thr	His	Gly	Gln	Val	Gly	Thr	Arg	Arg	Tyr	Met	Ala	Pro
	355					360						365			
Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe	Gln	Arg	Asp	Ala	Phe	Leu	Arg
370					375						380				
Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val	Leu	Trp	Glu	Leu	Ala	Ser	Arg
385					390					395					400
Cys	Thr	Ala	Ala	Asp	Gly	Pro	Val	Asp	Glu	Tyr	Met	Leu	Pro	Phe	Glu
				405					410					415	
Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu	Glu	Asp	Met	Gln	Glu	Val	Val
			420					425				430			
Val	His	Lys	Lys	Lys	Arg	Pro	Val	Leu	Arg	Asp	Tyr	Trp	Gln	Lys	His
	435					440						445			
Ala	Gly	Met	Ala	Met	Leu	Cys	Glu	Thr	Ile	Glu	Glu	Cys	Trp	Asp	His
450					455						460				
Asp	Ala	Glu	Ala	Arg	Leu	Ser	Ala	Gly	Cys	Val	Gly	Glu	Arg	Ile	Thr
465					470					475					480
Gln	Met	Gln	Arg	Leu	Thr	Asn	Ile	Ile	Thr	Thr	Glu	Asp	Ile	Val	Thr
				485					490					495	
Val	Val	Thr	Met	Val	Thr	Asn	Val	Asp	Phe	Pro	Pro	Lys	Glu	Ser	Ser
			500					505					510		
Leu															

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Met	Thr	Ala	Pro	Trp	Ala	Ala	Leu	Ala	Leu	Leu	Trp	Gly	Ser	Leu	Cys
			5					10						15	
Ala	Gly	Ser	Gly	Arg	Gly	Glu	Ala	Glu	Thr	Arg	Glu	Cys	Ile	Tyr	Tyr
			20					25					30		
Asn	Ala	Asn	Trp	Glu	Leu	Glu	Arg	Thr	Asn	Gln	Ser	Gly	Leu	Glu	Arg
		35					40					45			
Cys	Glu	Gly	Glu	Gln	Asp	Lys	Arg	Leu	His	Cys	Tyr	Ala	Ser	Trp	Arg
	50					55					60				
Asn	Ser	Ser	Gly	Thr	Ile	Glu	Leu	Val	Lys	Lys	Gly	Cys	Trp	Leu	Asp
65					70					75				80	
Asp	Phe	Asn	Cys	Tyr	Asp	Arg	Gln	Glu	Cys	Val	Ala	Thr	Glu	Glu	Asn
			85						90					95	
Pro	Gln	Val	Tyr	Phe	Cys	Cys	Cys	Glu	Gly	Asn	Phe	Cys	Asn	Glu	Arg
			100					105					110		
Phe	Thr	His	Leu	Pro	Glu	Pro	Gly	Gly	Pro	Glu	Val	Thr	Tyr	Glu	Pro
		115					120						125		
Pro	Pro	Thr	Ala	Pro	Thr	Leu	Leu	Thr	Val	Leu	Ala	Tyr	Ser	Leu	Leu
		130				135					140				
Pro	Ile	Gly	Gly	Leu	Ser	Leu	Ile	Val	Leu	Leu	Ala	Phe	Trp	Met	Tyr
145					150					155				160	
Arg	His	Arg	Lys	Pro	Pro	Tyr	Gly	His	Val	Asp	Ile	His	Glu	Val	Arg
				165					170					175	
Gln	Cys	Gln	Arg	Trp	Ala	Gly	Arg	Arg	Asp	Gly	Cys	Ala	Asp	Ser	Phe
			180					185					190		
Lys	Pro	Leu	Pro	Phe	Gln	Asp	Pro	Gly	Pro	Pro	Pro	Pro	Ser	Pro	Leu
		195					200					205			
Val	Gly	Leu	Lys	Pro	Leu	Gln	Leu	Leu	Glu	Ile	Lys	Ala	Arg	Gly	Arg
	210					215					220				
Phe	Gly	Cys	Val	Trp	Lys	Ala	Gln	Leu	Met	Asn	Asp	Phe	Val	Ala	Val
225					230					235				240	
Lys	Ile	Phe	Pro	Leu	Gln	Asp	Lys	Gln	Ser	Trp	Gln	Ser	Glu	Arg	Glu
			245						250					255	
Ile	Phe	Ser	Thr	Pro	Gly	Met	Lys	His	Glu	Asn	Leu	Leu	Gln	Phe	Ile
			260					265					270		
Ala	Ala	Glu	Lys	Arg	Gly	Ser	Asn	Leu	Glu	Val	Glu	Leu	Trp	Leu	Ile
		275					280					285			
Thr	Ala	Phe	His	Asp	Lys	Gly	Ser	Leu	Thr	Asp	Tyr	Leu	Lys	Gly	Asn
		290				295					300				
Ile	Ile	Thr	Trp	Asn	Glu	Leu	Cys	His	Val	Ala	Glu	Thr	Met	Ser	Arg
305				310						315				320	
Gly	Leu	Ser	Tyr	Leu	His	Glu	Asp	Val	Pro	Trp	Cys	Arg	Gly	Glu	Gly
			325						330					335	
His	Lys	Pro	Ser	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Lys	Asn	Val	Leu
			340					345					350		
Leu	Lys	Ser	Asp	Leu	Thr	Ala	Val	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Val
		355					360					365			
Arg	Phe	Glu	Pro	Gly	Lys	Pro	Pro	Gly	Asp	Thr	His	Gly	Gln	Val	Gly
		370				375					380				
Thr	Arg	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Ala	Ile	Asn	Phe
385				390						395				400	
Gln	Arg	Asp	Ala	Phe	Leu	Arg	Ile	Asp	Met	Tyr	Ala	Met	Gly	Leu	Val
			405						410					415	
Leu	Trp	Glu	Leu	Val	Ser	Arg	Cys	Lys	Ala	Ala	Asp	Gly	Pro	Val	Asp
		420						425					430		
Glu	Tyr	Met	Leu	Pro	Phe	Glu	Glu	Glu	Ile	Gly	Gln	His	Pro	Ser	Leu



275	280	285
Thr Glu Lys Asp Ile Phe	Ser Asp Ile Asn Leu Lys	His Glu Asn Ile
290	295	300
Leu Gln Phe Leu Thr Ala	Glu Glu Arg Lys Thr	Glu Leu Gly Lys Gln
305	310	315
Tyr Trp Leu Ile Thr Ala	Phe His Ala Lys Gly	Asn Leu Gln Glu Tyr
325	330	335
Leu Thr Arg His Val Ile	Ser Trp Glu Asp Leu	Arg Lys Leu Gly Ser
340	345	350
Ser Leu Ala Arg Gly Ile	Ala His Leu His Ser	Asp His Thr Pro Cys
355	360	365
Gly Arg Pro Lys Met Pro	Ile Val His Arg Asp	Leu Lys Ser Ser Asn
370	375	380
Ile Leu Val Lys Asn Asp	Leu Thr Cys Cys Leu	Cys Asp Phe Gly Leu
385	390	395
Ser Leu Arg Leu Asp Pro	Thr Leu Ser Val Asp	Asp Leu Ala Asn Ser
405	410	415
Gly Gln Val Gly Thr Ala	Arg Tyr Met Ala Pro	Glu Val Leu Glu Ser
420	425	430
Arg Met Asn Leu Glu Asn	Ala Glu Ser Phe Lys	Gln Thr Asp Val Tyr
435	440	445
Ser Met Ala Leu Val Leu	Trp Glu Met Thr Ser	Arg Cys Asn Ala Val
450	455	460
Gly Glu Val Lys Asp Tyr	Glu Pro Pro Phe Gly	Ser Lys Val Arg Glu
465	470	475
His Pro Cys Val Glu Ser	Met Lys Asp Asn Val	Leu Arg Asp Arg Gly
485	490	495
Arg Pro Glu Ile Pro Ser	Phe Trp Leu Asn His	Gln Gly Ile Gln Met
500	505	510
Val Cys Glu Thr Leu Thr	Glu Cys Trp Asp His	Asp Pro Glu Ala Arg
515	520	525
Leu Thr Ala Gln Cys Val	Ala Glu Arg Phe Ser	Glu Leu Glu His Leu
530	535	540
Asp Arg Leu Ser Gly Arg	Ser Cys Ser Glu Glu	Lys Ile Pro Glu Asp
545	550	555
Gly Ser Leu Asn Thr Lys		
565		

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Leu Thr Gly Arg Val Gly Ser Gly Arg Phe Gly Asn Val Ser Arg Gly	5	10	15
Asp Tyr Arg Gly Glu Ala Val Ala Val Lys Val Phe Asn Ala Ile Asp	20	25	30
Glu Pro Ala Phe His Lys Glu Ile Glu Ile Phe Glu Thr Arg Met Leu	35	40	45
Arg His Pro Asn Val Leu Arg Tyr Ile Gly Ser Asp Arg Val Asp Thr	50	55	60
Gly Phe Val Thr Glu Leu Trp Leu Val Ile Glu Tyr His Pro Ser Gly	65	70	75
Ser Leu His Asp Phe Leu Leu Glu Asn Thr Val Asn Ile Glu Thr Tyr			80

	85		90		95
Tyr Asn Leu Met Arg Ser Thr Ala Ser Gly Leu Ala Phe Leu His Asn					
	100		105		110
Gln Ile Gly Gly Ser Lys Glu Ser Asn Lys Pro Ala Met Ala His Arg					
	115		120		125
Asp Ile Lys Ser Lys Asn Ile Met Tyr Lys Asn Asp Leu Thr Cys Ala					
	130		135		140
Ile Gly Asp Leu Gly Leu Ser Leu Ser Lys Pro Glu Asp Ala Ala Ser					
	145		150		155
Asp Ile Ile Ala Asn Glu Asn Tyr Lys Cys Gly Thr Val Arg Tyr Leu					
	165		170		175
Ala Pro					

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: 130 amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34

Thr Arg Leu His Leu Cys His Cys Ser Arg Glu Val Gly Cys Asn Ala					
	5		10		15
Arg Thr Thr Gly Trp Val Pro Gly Ile Glu Phe Leu Asn Glu Thr Asp					
	20		25		30
Arg Ser Phe Tyr Glu Asn Thr Cys Tyr Thr Asp Gly Ser Cys Tyr Gln					
	35		40		45
Ser Ala Arg Pro Ser Pro Glu Ile Ser His Phe Gly Cys Met Asp Glu					
	50		55		60
Lys Ser Val Thr Asp Glu Thr Glu Phe His Asp Thr Ala Ala Lys Val					
	65		70		75
Cys Thr Asn Asn Thr Lys Asp Pro His Ala Thr Val Trp Ile Cys Cys					
	85		90		95
Asp Lys Gly Asn Phe Cys Ala Asn Glu Thr Ile Ile His Leu Ala Pro					
	100		105		110
Gly Pro Gln Gln Ser Ser Thr Trp Leu Ile Leu Thr Ile Leu Ala Leu					
	115		120		125
Leu Thr					
	130				

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Asp Leu Lys Pro Glu Asn
5

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:  
Asp Leu Ala Ala Arg Asn  
5

(2) INFORMATION FOR SEQ ID NO: 37:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:  
Gly Thr Xaa Xaa Tyr Xaa  
5

(2) INFORMATION FOR SEQ ID NO: 38:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:  
Gly Thr Xaa Xaa Phe Xaa  
5

(2) INFORMATION FOR SEQ ID NO: 39:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
Gly Ser Xaa Xaa Tyr Xaa  
5

(2) INFORMATION FOR SEQ ID NO: 40:  
(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
Gly Ser Xaa Xaa Phe Xaa  
5

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 6 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: peptide  
    (v) FRAGMENT TYPE: internal  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:  
Xaa Pro Ile Lys Trp Thr  
    5

(2) INFORMATION FOR SEQ ID NO: 42:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 6 amino acids  
        (B) TYPE: amino acid  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
        (v) FRAGMENT TYPE: internal  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:  
Xaa Pro Ile Lys Trp Met  
    5

(2) INFORMATION FOR SEQ ID NO: 43:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 6 amino acids  
        (B) TYPE: amino acid  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
        (v) FRAGMENT TYPE: internal  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:  
Xaa Pro Ile Arg Trp Thr  
    5

(2) INFORMATION FOR SEQ ID NO: 44:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 6 amino acids  
        (B) TYPE: amino acid  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
        (v) FRAGMENT TYPE: internal  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
Xaa Pro Ile Arg Trp Met  
    5

(2) INFORMATION FOR SEQ ID NO: 45:  
    (i) SEQUENCE CHARACTERISTICS:  
        (A) LENGTH: 6 amino acids  
        (B) TYPE: amino acid  
        (D) TOPOLOGY: linear  
    (ii) MOLECULE TYPE: peptide  
        (v) FRAGMENT TYPE: internal  
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
Xaa Pro Val Lys Trp Thr  
    5

(2) INFORMATION FOR SEQ ID NO: 46:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (v) FRAGMENT TYPE: internal  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:  
Xaa Pro Val Lys Trp Met  
5

(2) INFORMATION FOR SEQ ID NO: 47:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (v) FRAGMENT TYPE: internal  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
Xaa Pro Val Art Trp Thr  
5

(2) INFORMATION FOR SEQ ID NO: 48:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: peptide  
 (v) FRAGMENT TYPE: internal  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
Xaa Pro Val Arg Trp Met  
5